

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:41:34 : Search time 75 Seconds

(without alignments)  
 950.521 Million cell updates/sec

Title: US-09-888-035A-2

Perfect score: 2722  
 Sequence: 1 MGMEVAARLGALYTSDYA.....GRGFVPPSPGSPTEQSHGGR 535

Scoring table: BL003662

Gapop 10.0

Gapext 0.5

Searched: 908470 seqs., 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_101002: \*

- 1: /SIDS2/gcgdata/geneseq/geneseq/geneseqp-emb1/AA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseq/geneseqp-emb1/AA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq/geneseqp-emb1/AA1982.DAT:\*
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- 20: /SIDS2/gcgdata/geneseq/geneseq/geneseqp-emb1/AA1999.DAT:\*
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- 22: /SIDS2/gcgdata/geneseq/geneseq/geneseqp-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq/geneseqp-emb1/AA2002.DAT:\*

#### ALIGNMENTS

RESULT	ID	Description
1	AAB11832	standard; Protein: 535 AA.
2	AAB11832	Rice Na+/H+ antiporter, OsNHX1.
3	XX	OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
4	AC	Oryza sativa.
5	XX	W0200037644-A1.
6	XX	29-JUN-2000.
7	XX	07-NOV-2000 (first entry)
8	XX	Rice Na+/H+ antiporter, OsNHX1.
9	XX	OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
10	XX	Oryza sativa.
11	XX	29-JUN-2000.
12	XX	07-NOV-2000 (first entry)
13	XX	Rice Na+/H+ antiporter, OsNHX1.
14	XX	OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
15	XX	Oryza sativa.
16	XX	29-JUN-2000.
17	XX	07-NOV-2000 (first entry)
18	XX	Rice Na+/H+ antiporter, OsNHX1.
19	XX	OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
20	XX	Oryza sativa.
21	XX	29-JUN-2000.
22	XX	07-NOV-2000 (first entry)
23	XX	Rice Na+/H+ antiporter, OsNHX1.
24	XX	OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
25	XX	Oryza sativa.
26	XX	29-JUN-2000.
27	XX	07-NOV-2000 (first entry)
28	XX	Rice Na+/H+ antiporter, OsNHX1.
29	XX	OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
30	XX	Oryza sativa.
31	XX	29-JUN-2000.
32	XX	07-NOV-2000 (first entry)
33	XX	Rice Na+/H+ antiporter, OsNHX1.
34	XX	OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
35	XX	Oryza sativa.
36	XX	29-JUN-2000.
37	XX	07-NOV-2000 (first entry)
38	XX	Rice Na+/H+ antiporter, OsNHX1.
39	XX	OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
40	XX	Oryza sativa.
41	XX	29-JUN-2000.
42	XX	07-NOV-2000 (first entry)
43	XX	Rice Na+/H+ antiporter, OsNHX1.
44	XX	OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
45	XX	Oryza sativa.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2722	100.0	535	Rice Na+/H+ antiporter, OsNHX1.
2	2105.5	77.4	555	Attlex_gmelini_N
3	2103.5	77.3	540	Protein regulating
4	2095.5	77.0	553	Protein regulating
5	2055.5	75.5	542	Protein regulating
6	2023.5	74.3	538	Arabidopsis thaliana
7	1966	72.2	555	Protein regulating
8	1852.5	68.1	547	Arabidopsis thaliana
9	1799.5	66.1	571	Arabidopsis thaliana
10	1550.5	57.0	556	Physcomtrella pat-

Human secreted protein  
 Human transporter

Human protein NOV6  
 Arabidopsis thaliana

Yeast SCNHX1 polyp

Human HSNE-6 poly

Gene #21 human sec

Human secreted pro

Human EST encoded

Herbically activ

Human secreted pro

Human secreted pro

Human albumin fusi

Human protein NOV6

Arabidopsis thalia

AtNHX1

Human EST encoded

Arabidopsis thalia

Novel human diagno



PN	WO200114560-A1.	AAB73253	standard; protein; 553 AA.
XX	01-MAR-2001.	XX	
PD	XX	AC	AAB73253;
XX	24-AUG-2000; 2000WO-JP05722.	XX	
PF	XX	DT	14-MAY-2001 (first entry)
PR	24-AUG-1999; 99JP-0236800.	XX	
XX	(SUNR ) SUNTORY LTD.	DE	Protein regulating the pH of vacuoles.
PA	XX	XX	
PI	Iida S, Tanaka S, Inagaki Y;	KW	Vacuole pH regulation; flower colour.
XX	XX	OS	Nierembergia hybrida.
DR	DR	XX	
N-PSDB; AAF75764.	WO200114560-A1.	PN	
XX	XX	XX	
PS	Example 7; Page 42-45; 68pp; Japanese.	PA	01-MAR-2001.
PT	Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in horticulture	PA	24-AUG-2000; 2000WO-JP05722.
PT	XX	PR	24-AUG-1999; 99JP-0236800.
PT	XX	XX	
SQ	Sequence 540 AA;	(SUNR ) SUNTORY LTD.	
Query	Match 77.3%; Score 2103.5; DB 22; Length 540;	PA	
Best Local Similarity	77.4%; Pred. No. 3,4e-207;	PS	Example 7; Page 50-52; 68pp; Japanese.
Matches	404; Conservative 53; Mismatches 62; Indels 3; Gaps 1;	XX	
CC	The present sequence is a protein, which has vacuolar pH regulatory activities. The protein enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The protein is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable in horticulture.	CC	The present sequence is a protein, which has vacuolar pH regulatory activities. The protein enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The protein is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable in horticulture.
CC	XX	CC	
CC	Sequence 540 AA;	CC	
Query	15 TTSDYASVVSINLFLVALCACIVLGHLLLEENRNWNNESTITALJIGLCTGVYILLMTKGKSS	DR	2001-191648/19
Db	16 STDHQSVSINLFLVALCACIVLGHLEENRNWNNESTITALVIGSGCTGIVILLSGKNS	DR	N-PSDB; AAF75765.
Qy	75 HLFVFSELFFIYLPLPPIFNGQVKKKQFRNEMTILEGAVTMISFTTISAAIAI 134	XX	
Db	76 HLFVFSELFFIYLPLPPIFNGQVKKKQFRNEMTILEGAVTMISFTTISAAIAI 135	XX	
Qy	135 FSRMNIGLTDVGDFELATGAIFSATDSVCTLQVLNQDETFLYSLVGEGVVNDAVISVLF 194	SO	Sequence 553 AA;
Db	136 FKMNNIGLSEIGDLYAIGAIFSATDSVCTLQVLNQDETFLYSLVGEGVVNDAVISVLF 195	Query Match	77.0%; Score 2095.5; DB 22; Length 553;
Qy	195 NALQNFDLVHIDAVVLRKFLGNNFYFLSSTFLGVAGLSSAYIKKLYIGRHSRDEVA 254	Best Local Similarity	77.8%; Pred. No. 2.3e-206;
Db	196 NALQNFDLSHIDTGKAMLVNLFLYPLASSTALGVAGLSSAYIKKLYIGRHSRDEVA 255	Matches	49; Mismatches 63; Indels 3; Gaps 1;
Qy	255 LMMEMAYLSYMLAELLDISGLTUVFFCGTIVMSHYTNWTESSRVTTKHAFATLSPTAET 314	Qy	15 TTSDYASVVSINLFLVALCACIVLGHLLLEENRNWNNESTITALJIGLCTGVYILLMTKGKSS
Db	256 IMTLMAYLSYMLAELFYSATLUVFFCGTIVMSHYTNWTESSRVTTKHAFATLSPTAET 315	Db	16 STDHQSVSINLFLVALCACIVLGHLEENRNWNNESTITALVIGSGCTGIVILLSGKNS
Qy	315 FFLYVGMDALDIEKWEFASDRPKGSIGTSSLLGLVLIGRAAEVPLPSELNSLTKKAPN 374	Qy	15 FSRMNIGLTDVGDFELATGAIFSATDSVCTLQVLNQDETFLYSLVGEGVVNDAVISVLF 194
Db	316 FFLYVGMDALDIEKWKVSDSPG1SYVSSFLGVGRAEVPLPSELNSLTKKPE 375	Db	16 HLFVFSELFFIYLPLPPIFNGQVKKKQFRNEMTILEGAVTMISFTTISAAIAI 134
Qy	375 EKITWROQVVIWAGLGMGAVSIALAYNKFTPSGHTOLHGNAIMTISTITVLFSTMVFG 434	Qy	17 HLFVFSELFFIYLPLPPIFNGQVKKKQFRNEMTILEGAVTMISFTTISAAIAI 135
Db	376 AKTSFNQQVTIWAGLGMGAVSMALYNQFTRGHTQLRANRIMITSTTVLFSTVFG 435	Db	17 HLFVFSELFFIYLPLPPIFNGQVKKKQFRNEMTILEGAVTMISFTTISAAIAI 135
Qy	435 MMTPKPLRILLPLPSGH - - PVSPEPSSPKSKLHSPLSPTMGGDLESTNTYRPPSSRLML 491	Qy	18 HLFVFSELFFIYLPLPPIFNGQVKKKQFRNEMTILEGAVTMISFTTISAAIAI 135
Db	436 LMTPKPLRILLPLPSHKHLRMSSEPTPKSFIVPLLDSTDSEADLERHVDPHSLRMLL 495	Db	19 HLFVFSELFFIYLPLPPIFNGQVKKKQFRNEMTILEGAVTMISFTTISAAIAI 135
Qy	492 TKPHTHTVHYWWRKFDDALMRPMGGRGFVFPSPGSPTEQSNG 533	Qy	196 NAVQNPDLSHIYSTGKALQLIGNFLYFAASSPFLGVAVGLSSAFIKKKLFGRAHSRDEVA
Db	496 STPSHTVHYWWRKDNDATMRPYEGGRGEVFPAGSPSTDPPVGG 537	Qy	20 HLFVFSELFFIYLPLPPIFNGQVKKKQFRNEMTILEGAVTMISFTTISAAIAI 135
Qy	375 EKTRWROQVVIWAGLGMGAVSIALAYNKFTPSGHTOLHGNAIMTISTITVLFSTMVFG 434	Db	21 HLFVFSELFFIYLPLPPIFNGQVKKKQFRNEMTILEGAVTMISFTTISAAIAI 135

Db 376 DKISFNQQTIVWAGLIMRGAVSMALAYNQFTRGGHTQLRANAIMITSTITVLFSTVVFG 435  
 Qy 435 MMTKPLIPLLIPASGH--PVTSESPSKPSKSHSPSPLTSMQGSDLESTTNIVRPSSRLML 491  
 Db 436 LMTKPLIPLLIPSKHLMRMSSEPMTPKPSKSHPLADSTOSEADLGRHRPHSLRMLL 495  
 Qy 492 TPKPTHTHYWYWRKEDDALMRPMFGRGFVPPFSPGSPTE 529  
 Db 496 STPSHTVHYWYWRKEDNAFMRFVFFGRGFVPPFVGSPTE 533

**RESULT 5**  
**AAB73251** standard; protein: 542 AA.  
 XX AAB73251;  
 AC  
 XX DT 14-MAY-2001 (first entry)  
 XX DE Protein regulating the pH of vacuoles.  
 RW Vacuole pH regulation; morning glory; flower colour.  
 XX CS Ipomoea nil.  
 XX PN WO200114560-A1.  
 XX PD 01-MAR-2001.  
 XX PF 24-AUG-2000; 2000WO-JP05722.  
 PR 24-AUG-1999; 99JP-0236800.  
 XX PA (SUNR ) SUNTRY LTD.  
 PI Iida S, Tanaka S, Inagaki Y;  
 XX WPI; 2001-191648/19.  
 DR N-PSDB; AAF7552.  
 XX PT Morning glory originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in horticulture -  
 XX PS Claim 2; Page 30-33; 68pp; Japanese.  
 CC The present sequence is a protein from Morning Glory, which has vacuolar pH regulatory activities. The protein enables flower colour to be controlled via regulation of the vacuolar pH. Colours can range from blue to red in colour spectrum. The protein is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable in horticulture.  
 XX SQ Sequence 542 AA;

Query Match 75.5%; Score 2055.5; DB 22; Length 542;  
 Best Local Similarity 76.4%; Pred. No. 2.9e-202; Mismatches 49; Gaps 3;

Db 16 TSDYASVWSINRVALAACIVLGHLLERNWYNESITALIGLCTGVWLMTKGKSSH 75  
 Qy 16 TSDYASVWSINRVALAACIVLGHLLERNWYNESITALIGLCTGVWLMTKGKSSH 75  
 Db 16 TSDYASVWSINRVALAACIVLGHLLERNWYNESITALIGLCTGVWLMTKGKSSH 75  
 Qy 76 LFEVESDLEFFYLPLPILFNAGFOVKKOFFRNEMTITLGAYGTMISFTISTAAIF 135  
 Db 76 LFEVESDLEFFYLPLPILFNAGFOVKKQFFVNEMTITLGAYGTLISCSISFGAVKIF 135  
 Qy 136 SRMNIGLTDVGDFLAIGAIFSATDSVCTLQVINQDETFLYSLVFGVWMDATSVLFN 195  
 Db 136 KHLDDFLDFGDYLAIGAFTAATDSVCTLQVLQSDETFLYSLVFGESVNDATSVLFN 195

RESULT 6  
 AAY40901  
 ID AAY40901 standard; protein; 538 AA.

XX AC AAY40901;  
 XX DT 18-JAN-2000 (first entry)

XX DE Arabidopsis thaliana Na/H transporter AtNHX1.

XX KW Sodium; proton; antiport; transporter; salt tolerance; salt management; transgenic plant; survival; soil; farming; accumulation; irrigation; crop.

XX OS Arabidopsis thaliana.

XX PN WO9947679-A2.

XX PD 23-SEP-1999.

XX PA 18-MAR-1999; 99WO-CA00219.

XX PR 18-MAR-1999; 98US-0078474.

XX PR 15-JAN-1999; 99US-011611.

XX PA (BLUM/) BLUMWALD E.

PA (APSE/) APSE M.

PA (SNED/) SNEDDEN W.

PA (AHAR/) AHARON G.

XX PI Blumwald E, Apse M, Snedden W, Aharon G;

XX DR WPT; 1999-571840/48.

DR N-PSDB; AAZ222591.

XX PT Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants -

XX PS Claim 36; Fig 1A; 93pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a plant Na/H transporter polypeptide, or a fragment

CC and capable of increasing salt tolerance in a cell. This sequence

CC corresponds to the AtNHX1 transporter from *Arabidopsis thaliana*.

CC The Na/H transporter polypeptides provide a means of intracellular

CC salt management, particularly in plants. The sequences are useful for

CC producing transgenic plants that are capable of surviving in soil with

CC high salt levels that would normally inhibit growth of the crop species.

This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops, such as potatoes, tomatoes, brassica, cotton, sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley, artriplex, sorghum, alfalfa, saicornia and others would benefit from increased salt tolerance.

CC	PA (SUNR ) SUNTRY LTD.
CC	XX Tida S , Tanaka S , Inagaki Y;
CC	PI XX
CC	PPL: 2001-191648/19.
CC	DR N-PSDB; AAF75766.
CC	XX
CC	Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in horticulture -
XX	PT
SQ Sequence 538 AA:	Example 7 ; Page 57-60; 68pp; Japanese.
Query Match 74.3%; Score 2023.5; DB 20; Length 538;	PT
Best Local Similarity 73.3%; Pred. No. 5.6e-199; Mismatches 60; Indels 3; Gaps 2;	PT
Matches 389; Conservative 60; Indels 79; Gaps 5;	PS
Db 3 MEVANAROGALYPTSDYASVVSINFLALLCAGTCIVLHLLNEENRTWNESITALLIGLCTG 62	PS
Db 2 LDSLVSKPLSL-STSDHSVAVNLNEFLALLCAGTCIVLHLLNEENRTWNESITALLIGLCTG 60	PS
Qy 63 VVILLMTKGKSSHLEFVFSDELFLFLPPTIFNAGFOVKKOFFRNEMTIPLEFGAVGTM 1.22	PS
Db 61 VTIILISCKSSHLVLFDELFLFLPPTIFNAGFOVKKOFFRNEMTIPLEFGAVGTM 120	PS
Qy 123 SFFTTISIAAIAIFSRMNIGTLDYDFLAIAGAIFSATDVCUTLQVNDETPLFLYSLVGE 182	Sequence 555 AA:
Db 121 SCTTISGVTQFFKKLDDFGDYLAIAGAIFAAATDVCUTLQVNDETPLFLYSLVGE 180	Query Match 72.2%; Score 1966; DB 22; Length 555;
Qy 183 GVNDATSTVLFNALQNDLVLHDAVNLKLGNNFYFLFSLSTFLGFAGNLSSAYIKKL 242	Best Local Similarity 71.38%; Pred. No. 4.8e-193; Mismatches 55; Indels 18; Gaps 5;
Db 181 GVNDATSVYVENIAQSFLTHLNHEAFLGLNFNLFLJLSTLGAATGLISAYIKKL 240	Matches 390; Conservative 55; Indels 18; Gaps 5;
Qy 243 YGRHSTDREVALMMLMAYLSYMAELDLGSLLTFLVFCGTGIVMSHYTWHTWHTTESSRTTK 302	Qy 1 MGME ---VAARLGLALYTTSYASVVSINFEVALLCACTIVLGHLEENRWNESITALLI 56
Db 241 YGRHSTDREVALMMLMAYLSYMAELDLGSLLTFLVFCGTGIVMSHYTWHTWHTTESSRTTK 300	Db 1 MGFEVSKLAASETDNW-SSGGHSVVAITLFLVTLCTIVGHLEENRWNESITALLI 59
Qy 303 HAFTATLSPFAETFLFLYGMDALDEKEWFAFPGKSIGISSITLGLVLTGRAAFVPL 362	Qy 57 IGLCTGVVILIMTKGKSSHLEFVFSDELFLFLPPTIFNAGFOVKKOFFRNEMTIPLEFG 116
Db 301 HAFTATLSPFAETFLFLYGMDALDIDKRSVSDTPGTGTSIAVSSLIMGLVLTGRAAFVPL 360	Db 60 IGLATGVILLISGKSSHLLVFSDELFLFLPPTIFNAGFOVKKOFFRNEMTIPLEFG 119
Qy 363 SEISNLTKKAPNEKITWROQQVVIWAGLMRAVIALAYNKFRSGTHTOLHGNAIMTST 4.22	Qy 117 AVGMISFFTISIAIAIFSRMNIGTLDYDFLAIAGAIFATDSVCTQLVNDETPLFLY 176
Db 361 SFSLNLAKKNOSEKINFNHQVVIWAGLMRAVIALYNGKFRSGTHTOLHGNAIMTST 4.20	Db 120 AVGLTISLIIISLGTIAFFPKNMN-RLVGVDLIALGIAIFAAATDSCUTLQVLSQDETPLLY 178
Qy 423 ITVVLFLSTMYFGMMTKPLIRLPLLPAKGHPV- -SEPSSPKSLHSPLTSMQGSDLESTMN 4.80	Qy 177 SLVYEGCVNDATSVLFLNQDLYHIDAAVVKFLGFLFYLISLSTFEGVFGCVAGLSSA 236
Db 421 ITVCLFLSTVFGMMTKPLIRLPLLPAKGHPV- -SEPSSPKSLHSPLTSMQGSDLESTMN 4.80	Db 179 SLVYEGCVNDATSVLFLNQDLYHIDAAVVKFLGFLFYLISLSTFEGVFGCVAGLSSA 238
Qy 481 IVRPSLRLMLTAKPTHTVHYWRFDDALMRPMFGGRRVPPSPGPBQS 531	Qy 237 YIJKLYIGRHSTDREVALMMLMAYLSYMAELDLGSLLTFLVFCGTGIVMSHYTWHTWHTTES 296
Qy 481 VPRPDSTRGFLTRPTVHYWRFDDALMRPMFGGRRVPPGPSPTERN 531	Db 239 YIJKLYIGRHSTDREVALMMLMAYLSYMAELDLGSLLTFLVFCGTGIVMSHYTWHTWHTEN 298
Db 481 VPRPDSTRGFLTRPTVHYWRFDDALMRPMFGGRRVPPGPSPTERN 531	Qy 297 SRVTKHAFATLSPFAETFLFLYGMDALDEKEWFAFPGKSIGISSITLGLVLTGRA 356
RESULT 7	Db 299 SRVTKHAFATLSPFAETFLFLYGMDALDEKEWFAFPGKSIGISSITLGLVLTGRA 358
AAB7354	Qy 357 AFVFPFLSNTUKAENEKTTWQOQVVIWAGLMRAVIALAYNFRSGTHTOLHGNA 4.16
ID AAB73254 standard; Protein: 555 AA.	Db 359 AFVFPFLSNTULAKSPTEKISLQQIWIWAGLMRAVIALAYNFRSGTHTOLHGNA 4.18
XX	Qy 417 IMTISTIVLFLSTMFGMMTKPLIRLPLLPA- -GHPTSESPSPKSLHSPL----- 466
AC AAB73254;	Db 419 IFITSTIVLFLSTVFLGMLTPIPLNLLPSKLNRSSEPTNSITIPLGEOSDV 478
XX	Qy 467 -LTSMOODLESTNTIVRPSLRLMLTAKPTHTVHYWRFDDALMRPMFGGRRVPPGPBQS 524
DT 14-MAY-2001 (first entry)	Db 479 AELFSTIRGOTSGGEPYARPSLRLMLTAKPTHTVHYWRFDDALMRPMFGGRRVPPGPBQS 538
XX	Qy 525 GSPEQS 531
DE Protein regulating the pH of vacuoles.	Db 539 GSPEERS 545
XX	AC AAY40905 ;
KW Vacuole pH regulation; flower colour.	XX AAY40905 ;
XX	AC AAY40905 ;
OS Torenia hybrida.	XX AAY40905 ;
XX	AC AAY40905 ;
PN WO200114560-A1.	XX AAY40905 ;
XX	AC AAY40905 ;
PD 01-MAR-2001.	XX AAY40905 ;
XX	AC AAY40905 ;
PF 24-AUG-2000; 2000WO-JP05722.	XX AAY40905 ;
XX	AC AAY40905 ;
PR 24-AUG-1999; 99JP-0236800.	XX AAY40905 ;
XX	AC AAY40905 ;

XX DT 18-JAN-2000 (first entry)

XX DE Arabidopsis thaliana Na/H transporter.

XX KW Sodium; proton; antiport; transporter; salt tolerance; salt management; transgenic plant; survival; soil; farming; accumulation; irrigation;

XX KW crop.

XX OS Arabidopsis thaliana.

XX PN W09947679-A2.

XX PD 23-SEP-1999.

PF 18-MAR-1999; 99WO-CA000219.

PR 18-MAR-1998; 98US-0078474.

PR 15-JAN-1999; 99US-0116111.

XX PA (BLUMWALD) BLUMWALD E.

PA (APSE) APSE M.

PA (SNED) SNEDDEN W.

PA (AHAR) AHARON G.

PI XX DR 1999-571840/48.

DR N-PDB; AA22595.

XX PT Nucleic acid molecules encoding sodium/proton transport polypeptides,

PT useful in genetic engineering salt tolerance in crop plants.

PS XX Claim 50: Fig 5A-B; 93pp; English.

CC The invention relates to an isolated nucleic acid molecule encoding a plant Na/H antiport (PNX) transporter polypeptide, or a fragment CC and capable of increasing salt tolerance in a cell. This sequence corresponds to a transporter from Arabidopsis thaliana.

CC The Na/H transporter polypeptides provide means of intracellular salt management, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops such as potatoes, tomatoes, brassica, cotton, sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley, atriplex, sorghum, alfalfa, salicornia and others would benefit from increased salt tolerance.

XX Sequence 547 AA;

Query Match 68.1%; Score 1852.5; DB 20; Length 547;

Best Local Similarity 72.3%; Pred. No. 2.2e-181;

Matches 361; Conservative 55; Mismatches 76; Indels 3; Gaps 2;

QY 3 MEVAARLGAATTSYASVSVINLFLVALICACTIVLGHILEENRWNESITALLIGCTG

Db 2 LDSLVSKLPSL-STSDHASVNLFLVALICACTIVLGHILEENRWNESITALLIGCTG

QY 63 VVILLMTKRSKSHFVFSEDLFFYLPLPPTENAGFOVKKKOFFRNFMLTLEFGAVGTM 122

Db 61 VTIILISKGSKSHLVLFSDELFYLPLPPTENAGFOVKKKOFFRNFMLTLEFGAVGTM 120

QY 123 SFTFTISIAIAIFSRMNIGLTVDGFDFLAIGAIFSATDSVCTQLVNQDETFLYSLVGE 182

Db 121 SCTTISLGTVQQFKKLIDCIGFLGDDYLAIGAIFAATDSVCTQLVNQDETFLYSLVGE 180

QY 183 GVNDATSLVFLNALQNFDLVHDAAVVFLGAGLNFYFLFLLGAATGLISAYVIKKL 242

Db 181 GTVNDATSLVFLNALQNFDLVHDAAVVFLGAGLNFYFLFLLGAATGLISAYVIKKL 240

QY 243 YIGRHSTDREVALMMAYLSYMLAELLDLSGLTTFGGTIVMSHYTWHNVTESSRVTTK 302

Db 241 YFGRHSTUREVALMMAYLSYMLAELLDLSGLTTFGGTIVMSHYTWHNVTESSRVTTK 300

QY 303 HAFATLSEFAETEFLYGM DALDIEKWEFAASDRPGKSIGISSILLGLVIGRAAFVPL 362

Db 301 HTATLSEFAETEFLYGM DALDIEKWEFAASDRPGKSIGISSILLGLVIGRAAFVPL 360

QY 363 SFLSNLTKKAPNEKTTWQOQVWWAGLMRGAVSIALAYNKETFRSGHTOLGNAIMTST 422

Db 361 SFLSNLAKKNQSEKINFNQVWWSLGRGAVSMALAYNKETFRAGTIDVRGNAIMTST 420

QY 423 ITVVLFSTMVEGMMTKPILRLLPASHGPVT - SEPPSPKSLHSPLTSMQSDLESTTN 480

Db 421 ITVCLFLSTVVFGLTKPLJISYJLPHQNAATTSMISDDNPKPSTHIPLDQSDTEPSGNHH 480

QY 481 IVRPSSLEMILJTKPT 495

Db 481 VPRPDSTRGELTRPT 495

RESULT 9

AAU02882 standard; Protein: 571 AA.

ID AAU02882

XX AAU02882;

AC AAU02882;

XX DT 12-SEP-2001 (first entry)

XX DE Arabidopsis thaliana AtNHX1 polypeptide.

XX KW AtNHX1; tonoplast pyrophosphatase hydrogen ion translocating pump; Avp1; vacuolar pyrophosphatase; salt tolerance; sodium; calcium; manganese; lead; freeze tolerance; 35S promoter; saline soil; thale-cress.

XX OS Arabidopsis thaliana.

XX PN WC200133945-Al.

XX PD 17-MAY-2001

XX PF 10-NOV-2000; 20000WO-US30955.

XX PR 10-NOV-1999; 99US-0164808.

PR 10-AUG-2000; 2000US-026223.

PR 22-AUG-2000; 2000US-0644039.

XX PA (UYCO-) UNIV CONNECTICUT.

PA (WHED) WHITEHEAD INST.

XX PI Gaiola RA;

XX DR WPI; 2001-328862/34.

XX PT Transgenic plants with salt tolerance, drought and freeze resistance and increased yield and flower size comprise exogenous H<sup>+</sup> genes or increased vacuolar pyrophosphatase expression -

XX PS Example 1; Fig 6: 68pp; English.

CC The sequence represents an Arabidopsis thaliana AtNHX1 polypeptide which is a tonoplast pyrophosphatase hydrogen ion (H<sup>+</sup>) translocating pump. Transgenic plants can be made by transforming plant cells with exogenous tonoplast pyrophosphate driven H<sup>+</sup> pump genes and an exogenous nucleic acid encoding a protein, such as Avp1, which alters expression of vacuolar pyrophosphatase. Salt tolerance may be introduced into a plant via transformation of the cells to induce upregulation of vacuolar pyrophosphatase expression. Drought and/or freeze tolerance may also be introduced through transformation with DNA encoding a vacuolar H<sup>+</sup> translocating pump linked to a promoter such as the 35S promoter. These processes are useful for bioremediating soil and removing cations such as sodium, calcium, manganese and lead from soil or water which can





D	23-MAY-2002.	Qy	117 AVGTMISSEFTSISIAAIFSRNNIGITLVDGFPLAIGAFISATDSVCTQLVNLQ-DEEPFL 175
D	25-OCT-2001; 2001WO-US46055.	Db	249 VFGTSAFVVGGGYFLGQADVISKLNMNTDSFAFGSLISAVDPVATAIFNALHVDPVL 231
X	27-OCT-2000; 2000US-243989P.	Qy	176 YSLVFGGVNDATSVLFNALQNDLVHIDA---VVKPLGLNNFFYFLSSTFLGVFA 231
R	03-NOV-2000; 2000US-24504P.	Db	309 NMLVFGESTLNDAVSVLTNTAEGLTPKNSDVSGLQFLQALDYLKMEFGSAALGTLT 368
R	09-NOV-2000; 2000US-247673P.	Qy	232 GLLSATIILKKLYIGRHSTDREVALMMIMAYLSYMLAEUDLSSILTVFEGIVMSHYTHW 291
R	17-NOV-2000; 2000US-249651P.	Db	369 GLISALVYKLKHIDLRKTPSLEFGMMIIFAYLPYGLAGISLSGIMAILFSGIVMSHYTHW 427
R	01-DEC-2000; 2000US-252232P.	Qy	292 NTTESSRTVTKUAFATSFIAETFLVYGMDALDI-EKWEFASDRPGKSIGISIL-L 348
R	20-NOV-2000; 2000US-250790P.	Db	428 NLSPVTOJLMQQTTRVIAFLCETCVFAPGLTSFSPHKFE----ISFVINC1 476
X	(INCYT-) INCYTE GENOMICS INC.	Qy	349 GLVLIGRAAFVPLPSLFSLNLTAKPNEKITWROQQVVIWAGLIMRGAYSTALAYNKFTPSG 408
X	Tang YT, Yue H, Nguyen DB, Hafalia AJA, Elliott VS, Lu Y;	Db	477 VLVLGRAVNTPLSYLUNFR--DHXTPKMFIMFSGL-RGAPTYAL----DIEDAKARR 574
X	Walla NK, Yao MG, Baughn MR, Gandhi AR, Ding L, Sanjawala M;	Qy	409 HTQL--HGNAIMTSTTUVLFSTMYFGMMTKPLIRLPLLPSGHPTSEPSSSPKSLHSP 465
X	Ramkumar J, Arvizu C, Gietzen KJ, Lal PG, Azimzai Y, Khan FA;	Db	526 HLDEPMEKROLIGTTTIVVLFPLLLGGSTMPLIRL-----FDDALMRMFGGGS 518
X	Thangavelu K, Thornton M, Lu DAM, Tribouley CM, Warren BA;	Qy	466 LTTSMOGDLESTNTIVPSSLNMLTPEHTVHYWWK-----FDDALMRMFGGGS 518
X	Isom CH, Das D, Raumann BE, Policky JL, Kearney L;	Db	575 NKKDVNLSKTEKNGNTVESEHLSER-LTEEEYEAHYIRQDLKGFWVLDAYLNPFTRR- 632
X	WPI; 2002-4633570/49.	Qy	519 FVPFSPGSPTEQSHGR 535
X	N-PSDB; ABK83214.	Db	633 -----LTQEDLHGR 642
X	New transporters and ion channels (TRICH) polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of TRICH, e.g. immunological, muscular or renal disorders -	RESULT 13	AAB29621
X	Claim 1; Page 138-140; 178pp; English.	ID	AAB29621 standard; Protein; 608 AA.
X	The invention relates to human transporters and ion channels (TRICH) polypeptides, a naturally occurring amino acid sequence 90 % identical to TRICH, a biologically active fragment of TRICH or an immunogenic fragment of TRICH. Also included are an isolated polynucleotide encoding TRICH, a recombinant polynucleotide comprising a promoter sequence operably linked to the TRICH polynucleotide, a cell transformed with the recombinant polynucleotide, a transgenic organism comprising the recombinant polynucleotide, an isolated antibody that binds specifically to TRICH, and screening for compounds which bind to TRICH, modulate TRICH, modulate TRICH expression or are ant/agonists of TRICH. The polypeptides are useful for diagnosing, treating, and preventing transport, neurological, muscle, immunological disorders (e.g. scleroderma, systemic lupus erythematosus, allergies), cell proliferative disorders such as cancers (e.g. leukaemia, cervical or breast cancers), neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy, catatonia), endocrine disorders (e.g. diabetes, Graves' disease), gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. Good pasture's syndrome), viral, bacterial, fungal, parasitic, protozoal and helminthic infections, cardiovascular disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis) and many other diseases and disorders detailed in the specification. They can also be used in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transporters and ion channels. TRICH or its fragments may also be used in screening for compounds that specifically bind to and modulate the activity of TRICH. The polynucleotides can be used to create knock-in humanised animals or transgenic animals to model human disease. The present sequence represents a TRICH protein.	XX	AAB29621;
X	Sequence 671 AA;	AC	
SQ	Query Match 22.7%; Score 618; DB 23; Length 671;	XX	
	Best Local Similarity 31.28%; Pred. No. 2.6e-54;	DR	WPI; 2000-656323/63.
	Matches 174; Conservative 95; Mismatches 222; Indels 66; Gaps 16;	XX	N-PSDB; AAC95370, AAC95371, AAC95373.
	Sequence 671 AA;	PD	Claim 10; Page 891-893; 964pp; English.
	Query 2 GMEEAAARIGALYTTSDYASVVSINLVALICACTIVLGHLEENR-WYNESITALIGL 59	XX	The invention relates to novel cat flea (Ctenocephalides felis) nucleic acids which are expressed in hindgut and Malpighian tubule (HMT) tissue and nerve cord (INC) tissue. The invention also relates to t-
Db	129 GKPILPVGTQEQEQQEQQSGHTIFFSLVLAICLHLLTRYLRLPEPSAVVSGI 188	XX	Claim 10; Page 891-893; 964pp; English.
Qy	60 CTGVVILMKGKSSHL--FVFSSEDFLFLPPIPNAGFOVKKKOFFNFMITLFG 116	CC	Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea infestations -
Db	189 LMGAVIKLIEFKLANKKEEMRPNNFLLPPTEESG1SLHKGNFFONGSITLFA 248	CC	XX
	Sequence 671 AA;	PA	XX
	Query Match 22.7%; Score 618; DB 23; Length 671;	PI	XX
	Best Local Similarity 31.28%; Pred. No. 2.6e-54;	DR	XX
	Matches 174; Conservative 95; Mismatches 222; Indels 66; Gaps 16;	XX	XX
	Sequence 671 AA;	PS	XX
	Query 2 GMEEAAARIGALYTTSDYASVVSINLVALICACTIVLGHLEENR-WYNESITALIGL 59	PT	XX
Db	129 GKPILPVGTQEQEQQEQQSGHTIFFSLVLAICLHLLTRYLRLPEPSAVVSGI 188	PT	XX
Qy	60 CTGVVILMKGKSSHL--FVFSSEDFLFLPPIPNAGFOVKKKOFFNFMITLFG 116	PT	XX
Db	189 LMGAVIKLIEFKLANKKEEMRPNNFLLPPTEESG1SLHKGNFFONGSITLFA 248	PT	XX

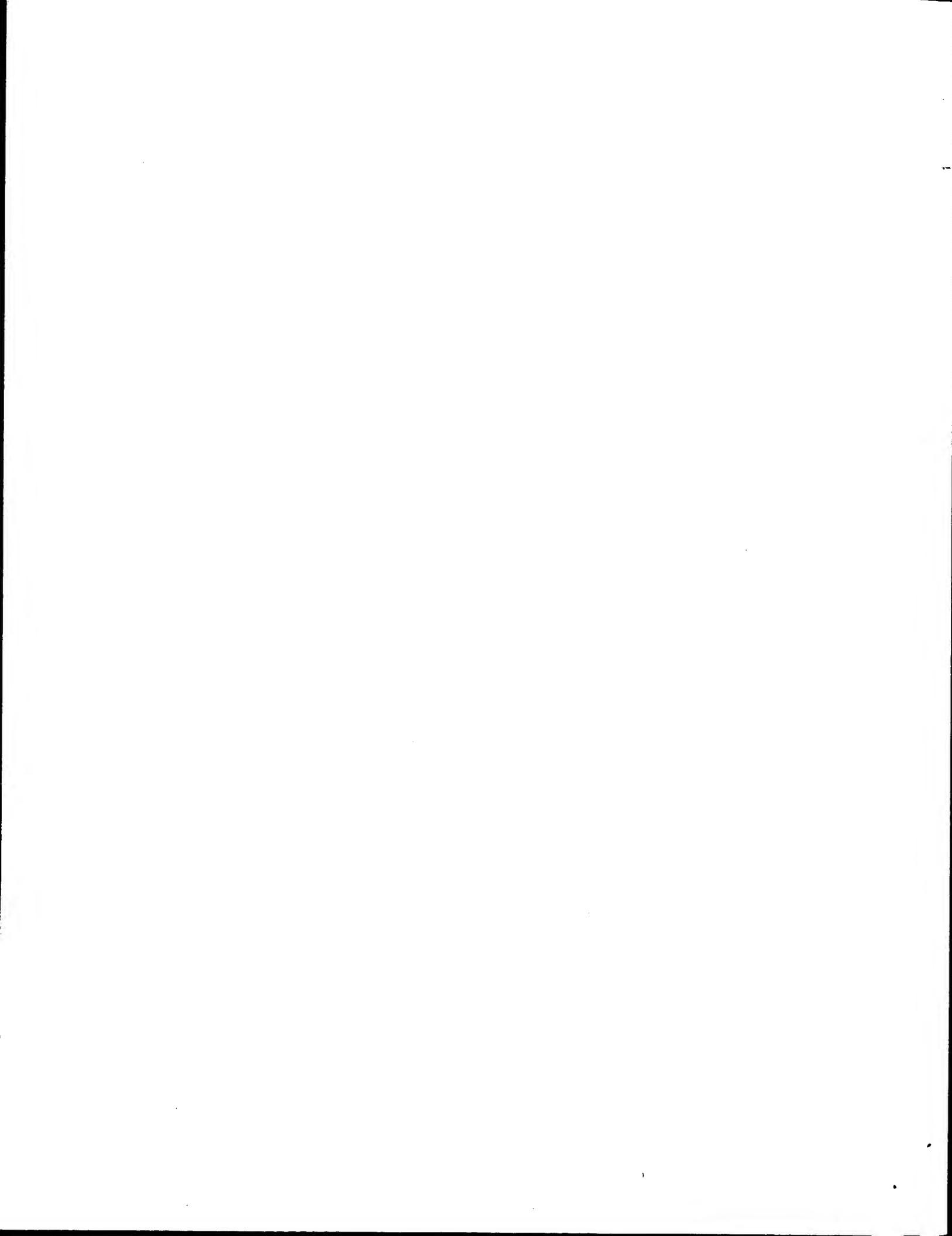
encoded proteins. The invention additionally encompasses expression constructs, recombinant viruses and recombinant cells comprising the nucleic acids of the invention, recombinant production of the proteins, antibodies against the proteins, a method of identifying inhibitors of the proteins, and compositions comprising the inhibitors for administration to an animal. The nucleic acids, and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with flea infestations. For example, the nucleic acids may be used to produce an HMT or HNC protein according to standard recombinant DNA methodology by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The HMT and HNC nucleic acids may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat flea or other homologous nucleic acid sequences in samples. They may also be used to study the expression and function of the proteins and their role in metabolism. The HMT and HNC proteins may be used as antigens in the production of specific antibodies, and in assays to identify modulators (agonists and antagonists) of HMT and/or HNC protein expression and activity. The anti-HMT/HNC protein antibodies and antagonists may also be used to downregulate protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of flea polypeptides in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The present sequence represents a cat flea HMT protein of the invention.

Sequence 608 AA;

Query Match	22.1%	Score 600.5;	DB 21;	Length 608;	
Best Local Similarity	35.1%	Pred. No. 1.4e-52;			
Matches	153;	Mismatches	153;	Gaps	13;
Qy	21	SVSINFLVALCAGTIGHLEEN -	-RWNVESTITALIGLCTGVILLMTKGSSHL -	76	
Db	81	SMSMFFVLCVALGILLHFMQLTGQYLPESIVVVFGALIGLILNMMSKNTANWN	N 140		
Qy	77	-FVFSEDLFLFYLPLPIIFNAGFOVKKKOFFRFNMFITLFGAVGTMSIFETISTAAIAF	135		
Db	141	EEAFSTAFFFLVLLPLPIIESGYNLHKGNFQNQGSILVFAIFGTAISAFVVG AGVYL	199		
Qy	136	SRNNIG-TLDVGDFLAIGSATDSVCTLQLVHQ-DENPVFLYSLVFGGVNDATSIYL	193		
Db	200	GMADAYNLSFVESPAFGSLSIADPVAIAFIALDYPVLANLVFGTSILNDAISIVL	259		
Qy	194	FNA-LQNFDLVHDAAVVULKFLGNPFYFLPLSFLTGFAGLSSAYIKKLYIGRHSTDRE	252		
Db	260	TAVLESNNPLMTAAEVSGLNRFCLMFEASAGIVYFAISALLKHVDLKRYPS-LE	318		
Qy	253	VALMMIAYSYMLAELLDLSGLITVFRGTVNHYTHNTESSRVITKHAPATLSFTA	312		
Db	319	LGMMLVFTYAPVLAEGTHLSGMAILFGIVNHYTHNLFNLYTQIMQTMRTLAFTA	378		
Qy	313	ETFLFLYVGMDALDIKEWFAASDPGKSIGISSLGGVLIGRAAFVPLSFLSNLTKKA	372		
Db	379	ETCVFAYLGMAIFFR----HRVEPALVWSLV -LCLIGRAANIPLSLVNQFRE-	429		
Qy	373	PNEKITWROQVIWAGLMRGAVSTIALA --- YNKFTFRSGHTQLHGNAIMITSITYVLF	428		
Db	430	-HKTKNAFMWFSGL-RGAYSALSLEHFSDETRH-----VITTTLIVLC	477		
Qy	429	STMYFGMMATKPLIRLL 444			
Db	478	TTLIFGGATMPLLKFL 493			
RESULT 14					
ID	ABB59364	standard; Protein;	649 AA.		
XX					
AC	ABB59364;				
DT	26-MAR-2002	(first entry)			
DE	Drosophila melanogaster	polypeptide	SEQ ID NO 4884.		
XX					

CC	KW	Drosophila; developmental biology; cell signalling; insecticide;			
CC	KW	pharmaceutical.			
CC	XX				
CC	OS	Drosophila melanogaster.			
CC	XX				
CC	PN	WO200171042-A2.			
CC	XX				
CC	PD	27-SEP-2001.			
CC	XX				
CC	PF	23-MAR-2001; 2001WO-US09231.			
CC	XX				
CC	PR	23-MAR-2000; 2000US-191637P.			
CC	PR	11-JUL-2000; 2000US-0614150.			
CC	XX				
CC	PA	(PEKE ) PE CORP NY.			
CC	XX				
CC	PI	Venter JC, Adams M,			
CC	PI	Li PWD, Myers EW;			
CC	XX				
CC	DR	WPI; 2001-656860/75.			
CC	DR	N-PSDB; ABL03467.			
CC	XX				
CC	PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.			
CC	PT				
CC	PT				
CC	XX				
PS	PS	Disclosure; SEQ ID NO 4884; 21pp + Sequence Listing; English.			
XX	XX				
CC	CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1676-ABU30511), expressed DNA sequences (ABL01840-ABL1675) and the encoded proteins (ABL1676-ABU30511).			
CC	CC	(ABL16737-ABU72072).			
CC	CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.			
XX	XX				
SQ	Sequence	649 AA;			
Query	Match	21.9%;	Score 595.5;	DB 22;	Length 649;
Best	Local Similarity	35.1%;	Mismatches	35-52;	
Matches	155;	Conservative	88;	Mismatches	155;
Db	101	SLSLFV-WICV-IMIGLILHSMLOQTGFQYLPESTVVFGAFIGLSNVMSGNSWKR	158		
Qy	24	SINLVEFLDFFLFYLPLPPIFNAGFOVKKKOFFRFNMFITLFGAVGTMSISFTTIAIAF	135		
Db	101	RWNESTITALIGLCTGVILLMTKGSSHL - KGKSSH	75		
Qy	76	LFVFSEDLDFFLFYLPLPPIFNAGFOVKKKOFFRFNMFITLFGAVGTMSISFTTIAIAF	135		
Db	159	EVEVSPMGFLVLPPIFESGYNHKGFFQFNGTIVLWVAFGTTKHFATLSF	217		
Qy	136	SRMWIG-TLDVGDFLAIGLISATDSVCTLQLVNAQ-DETPFLYSLVFGGVNDATSVL	193		
Db	218	GLGEVAFRLSFSESAFGSLISAVDPVATAFHLDWIPILNMUVFESTILNDAISIVL	277		
Qy	194	FINALDNFLVHDDA--VWLKGFLGNFLPFLSTFLGFLAYTCKKHFATLSF	250		
Db	278	TASITQSANVAEASTGEMPSALKTECAMFASAGIVYFAISLILKHIDLRKHP	336		
Qy	251	REVALMLMAYLSYMLAELLDLSGLTLYFECGIVMSHTIWHNTESSRVTTKHFATLSF	310		
Db	337	LEFAAMMLFAYVLAETIHLSSIMAFLFCGIVMSHTIWHNTESSRVTTKHFATLSF	396		
Qy	311	TAETFLFLYVGMDALDIKEWFAASDRPGKSIGISSILLGLV - LIGRAAEVPLSFLSNL	368		
Db	397	IAEICVFLYGLTAIFSEK -----HOVELSFVIAVILCLGRACNIFPLAFLVN	445		
Qy	369	TKAPNEKLTWROQVIWAGLMRGAVSIALANFKFTSGHTQLHGNAA---IMITSTIV	425		
Db	446	-KFREHKLNKRMQFIMWFSGL-RGAISYAL-----SLHNLNDSQEKRVVLTITLII	495		

Qy	426 VLFSTMYFGMMTKPLIRLLLP 446	CC palsy, amyotrophic lateral sclerosis; neurological (Alzheimer's disease, amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's muscular dystrophy); immunological (AIDS, Addison's disease, allergies, asthma); cell proliferative disorders (cancers, leukaemia, psoriasis); cardiac disease (angina, hypertension, or bradycardia) and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transporters and ion channels.
Db	496 VLEFTIVLGGTMMPLKLYKLKP 516	CC The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which TRICH expression may be correlated with a disease, to generate hybridization probes for mapping naturally occurring genomic sequence, and in drug screening. The present sequence is human TRICH-7 protein.
RESULT 15		
ID	AAE16770 standard; Protein; 673 AA.	
XX		
AC	AAE16770;	
XX		
DT	09-APR-2002 (first entry)	
XX		
DE	Human transporter and ion channel-7 (TRICH-7) protein.	
XX		
KW	Human; transporter and ion channel-7; TRICH-7; neuroprotective; asthma; noctropic; cytosolic; cardiovascular; immunosuppressive; cardionyopathy; antiinflammatory; protein therapy; akinesthesia; cystic fibrosis; leukaemia; Bell's palsy; amyotrophic lateral sclerosis; Alzheimer's disease; cancer; amnesia; dementia; myocarditis; Duchenne's muscular dystrophy; AIDS; Acquired Immune Deficiency Syndrome; Addison's disease; allergy; angina; cell proliferative disorder; psoriasis; cardiac disease; hypertension; bradycardia; gene expression; drug screening.	
XX		
OS	Homo sapiens	
XX		
FH	Location/Qualifiers	
Domain	19..38	
FT	/label= Transmembrane_domain	
FT	21..487	
FT	/note= "Sodium/hydrogen exchanger family domain"	
FT	155..173	
FT	/label= Transmembrane_domain	
FT	275..296	
FT	/label= Transmembrane_domain	
FT	457..477	
FT	/label= Transmembrane_domain	
XX	WO200192304-A2.	
XX	06-DEC-2001.	
PP	25-MAY-2001; 2001WO-US17065.	
XX		
PR	26-MAY-2000; 2000US-200424P.	
PR	01-JUN-2000; 2000US-20001P.	
PR	08-JUN-2000; 2000US-210588P.	
PR	16-JUN-2000; 2000US-213335P.	
PR	22-JUN-2000; 2000US-213747P.	
PR	29-JUN-2000; 2000US-213391P.	
XX	(INCY-) INCYTE GENOMICS INC.	
PA	Thornton M, Walia NK, Yue H, Nguyen DB, Lai P, Gandhi AR; Tribouley CM, Yao MG, Ramkumar J, Au-Young J, Lu Y, Tang YT; Azimzai Y, Bruns CM, Griffin JA, Yang J, Sanjanvala MS; Raumann BE, Lee EA, Rafaila A, Baughn MS, Green BD, Khan FA; Kearney L, Elliot VS, Sellhamer JJ, Policky JL, Borowsky ML; Burford N, Ding L, Lu DAM, Hillman JL;	
XX	WPI: 2002-122055/16.	
DR	N-PSDB; AAD27260.	
XX	New human transporters and ion channels (TRICH) polypeptides useful for diagnosing, treating or preventing disorders associated with aberrant expression of TRICH.	
XX	The invention relates to human transporters and ion channels (TRICH) polypeptides and their cDNA molecules. The nucleic acid and polypeptide sequences are useful in the diagnosis, treatment, and prevention of disorders associated with transport (akinesia, cystic fibrosis, Bell's	
PS	Claim 1; Page 151-153; 210pp; English.	
PS	The invention relates to human transporters and ion channels (TRICH) polypeptides and their cDNA molecules. The nucleic acid and polypeptide sequences are useful in the diagnosis, treatment, and prevention of disorders associated with transport (akinesia, cystic fibrosis, Bell's	
PT	PT	
PT	PT	
PT	PT	
XX	Search completed: March 26, 2003, 18:52:28	
XX	Job time : 77 secs	



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Scoring table:	BLOSUM62		
	Gapext 0.5		
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Total number of hits satisfying chosen parameters:	262574		
Minimum DB seq length:	0		
Maximum DB seq length:	2000000000		
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
	Listing first 45 summaries		
Database :	Issued_Patents_AA:*		
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	6: /cgn2_6/pktodata/1/iaa/backfile1.pep:*		
Pred.	No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
		SUMMARIES	
Result No.:	Score	Query Match Length DB ID	Description
1	4.91	18.0	832 2 US-09-677-734A-12 Sequence 12, Appl
2	4.91	18.0	832 4 US-09-097-053-12 Sequence 12, Appl
3	4.82.5	17.7	834 2 US-08-677-734A-9 Sequence 9, Appl
4	4.82.5	17.7	834 2 US-09-677-734A-10 Sequence 9, Appl
5	4.82.5	17.7	834 4 US-09-097-053-9 Sequence 10, Appl
6	4.82.5	17.7	834 4 US-09-097-053-10 Sequence 11, Appl
7	4.80.5	17.7	831 2 US-08-677-734A-11 Sequence 11, Appl
8	4.80.5	17.7	831 4 US-09-097-053-11 Sequence 11, Appl
9	200.5	7.4	683 4 US-09-134-001C-5576 Sequence 5576, AP
10	130.5	4.8	635 2 US-09-014-969-11 Sequence 11, Appl
11	124.5	4.6	605 4 US-09-134-001C-4425 Sequence 4425, AP
12	118.5	4.4	800 4 US-09-134-001C-5655 Sequence 5655, AP
13	114	4.2	477 4 US-09-134-001C-3487 Sequence 3487, AP
14	113	4.2	1394 4 US-09-213-053-2 Sequence 2, Appl
15	111	4.1	650 4 US-08-800-291B-4 Sequence 4, Appl
16	110	4.0	400 4 US-09-134-001C-2912 Sequence 2912, AP
17	109.5	4.0	617 4 US-09-134-001C-4012 Sequence 4012, AP
18	109	4.0	222 4 US-09-134-001C-4748 Sequence 4748, AP
19	109	4.0	649 4 US-08-800-291B-5 Sequence 5, Appl
20	108	4.0	649 4 US-08-800-291B-6 Sequence 6, Appl
21	107.5	3.9	492 4 US-09-134-001C-4847 Sequence 4847, AP
22	107	3.9	776 4 US-09-165-396-3 Sequence 3, Appl
23	104.5	3.8	518 4 US-09-134-001C-4744 Sequence 4744, AP
24	103.5	3.8	450 4 US-09-134-001C-4858 Sequence 4858, AP
25	103	3.8	324 4 US-09-134-001C-5525 Sequence 5525, AP
26	103	3.8	373 4 US-09-134-001C-4029 Sequence 4029, AP
27	103	3.8	405 4 US-09-134-001C-4999 Sequence 4999, AP

## ALIGNMENTS

Sequence 2, Appl

Sequence 4, Appl

Sequence 2, Appl

Sequence 5, Appl

Sequence 8, Appl

Sequence 4510, Ap

Sequence 2, Appl

Sequence 3, Appl

Sequence 2, Appl

Sequence 9, Appl

Sequence 5530, Ap

Sequence 5530, Ap

Sequence 3689, Ap

Sequence 3689, Ap

Sequence 4, Appl

Qy 25 INLFVALCACIVLGHLEE-NRWVNESITALLIIGCTGVVILLMTKGKSSH--FVFSE 81  
 Db 57 IALWVLVASLAKTIVFHLSHKTVSVPPASALLIVLGIVGGIVL---AHDIASFTLTP 111  
 Qy 82 DLFFTYLLPPIFNAGFOVKKKOFFERNFTMITLEFGAVGTMISFFTISIAAAIFSRMNIG 141  
 Db 112 TVEFFYLPLPPIVDAGFMPNRLFFNSLGSILYAVVGTWNNAATGSLYGVFLSGIMG 171  
 Qy 142 TLDVG - DFLAIGAIFATSVDCTQLVLNQ -DETPFLYSLAEGEVVVNDATSVLNFNALQ 198  
 Db 172 EKIGLDFDLFGLGSLIAAVDPAVLAFFEEHVNEVLFITFGESLINDATVVLXNVFQ 231  
 Qy 199 NFDLVHIDAAV --VLFKLGPNFYLFLSSTFUG-VFAGLLSAYIKRKYIGRHSTDREVA 254  
 Db 232 SPTVLGDKVTGVDCKVKGIVSFVVSLGGTLVGVVRAFLIS-LVTR-FTKHVRVTEPG 287  
 Qy 255 MMMLMAYLSYMELLDLSSLTIVFFCGIVMSHYTNWHNTBSSRVTTKHAFATLSFTAET 314  
 Db 288 FVFTISLPSYLTSEMISLSSSLAITPCGICQKYKANISSQSATVRYTMKMLASGAET 347  
 Qy 315 FLFLYYGMDALD - IEKWEAFTDRPGKSIGSSISLGLVGRAAFVPLSFLSNLKKA 372  
 Db 348 TIFMFLGISAIDPLINTWNTAFVR -----LTLFLFSVTRAIGCVLQTWLLNRYRMV 398  
 Qy 373 PNEKITWQQVTTIWAGLMRAVSIALAYNFTRSHQTLQIGNAT ---MTISTUTVVLF 428  
 Db 399 QLELI --DQVMSYGGL-REGAVAFALV -----ALLEGNKYKEKKNLKFVSTLIIIVF 445  
 Qy 429 STMVF-GMMTAKPLIR-LLLPAASGHPVTSSEPPSPKSLH 463  
 Db 446 FTVIQLGLTIKPLVQWLKVKESEH --REPKLNKEKLH 479

RESULT 2  
 US-09-097-053-12  
 ; Sequence 12, Application US/09097053  
 ; Patent No. 6392025  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brant, Steven R.  
 ; APPLICANT: Yun, Chris C.H.  
 ; APPLICANT: Donowitz, Mark  
 ; APPLICANT: Tse, Chung-Ming  
 ; TITLE OF INVENTION: Cloning, Tissue Distribution, and  
 ; Functional Analysis Of The Human Na+/H+ Exchanger Isoform,  
 ; NUMBER OF INVENTION: NHE3.  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 ; ADDRESS: 1300 I Street, N.W., Suite 700  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005-3315  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/097,053  
 ; FILING DATE:  
 ; CLASIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/677,734  
 ; FILING DATE: 10-JUL-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fordis, Jean B.  
 ; REGISTRATION NUMBER: 32,984  
 ; REFERENCE/DOCKET NUMBER: 05387-0043-00000  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 408-4000  
 ; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 832 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; POLARITY: linear  
; MOLECULE TYPE: Peptide  
; US-09-097-053-12  
; Query Match 18.0% ; Score 491; DB 4; Length 832;  
; Best Local Similarity 31.7%; Pred. No. 5.4e-39;  
; Matches 145; Conservative 88; Mismatches 172; Indels 52; Gaps 18;  
; Qy 25 INLFVALCACIVLGHLEE-NRWVNESITALLIIGCTGVVILLMTKGKSSH--FVFSE 81  
; Db 57 IALWVLVASLAKTIVFHLSHKTVSVPPASALLIVLGIVGGIVL---AHDIASFTLTP 111  
; Qy 82 DLFFTYLLPPIFNAGFOVKKKOFFERNFTMITLEFGAVGTMISFFTISIAAAIFSRMNIG 141  
; Db 112 TVEFFYLPLPPIVDAGFMPNRLFFNSLGSILYAVVGTWNNAATGSLYGVFLSGIMG 171  
; Qy 199 NFDLVHIDAAV --VLFKLGPNFYLFLSSTFUG-VFAGLLSAYIKRKYIGRHSTDREVA 254  
; Db 232 SPTVLGDKVTGVDCKVKGIVSFVVSLGGTLVGVVRAFLIS-LVTR-FTKHVRVTEPG 287  
; Qy 255 MMMLMAYLSYMELLDLSSLTIVFFCGIVMSHYTNWHNTBSSRVTTKHAFATLSFTAET 314  
; Db 288 FVFTISLPSYLTSEMISLSSSLAITPCGICQKYKANISSQSATVRYTMKMLASGAET 347  
; Qy 315 FLFLYYGMDALD - IEKWEAFTDRPGKSIGSSISLGLVGRAAFVPLSFLSNLKKA 372  
; Db 348 TIFMFLGISAIDPLINTWNTAFVR -----LTLFLFSVTRAIGCVLQTWLLNRYRMV 398  
; Qy 373 PNEKITWQQVTTIWAGLMRAVSIALAYNFTRSHQTLQIGNAT ---MTISTUTVVLF 428  
; Db 399 QLELI --DQVMSYGGL-REGAVAFALV -----ALLEGNKYKEKKNLKFVSTLIIIVF 445  
; Qy 429 STMVF-GMMTAKPLIR-LLLPAASGHPVTSSEPPSPKSLH 463  
; Db 446 FTVIQLGLTIKPLVQWLKVKESEH --REPKLNKEKLH 479  
; RESULT 3  
; US-08-677-734A-9  
; Sequence 9, Application US/08677734A  
; ; Patent No. 5871919  
; ; GENERAL INFORMATION:  
; ; APPLICANT: Brant, Steven R.  
; ; APPLICANT: Yun, Chris C.H.  
; ; APPLICANT: Donowitz, Mark  
; ; APPLICANT: Tse, Chung-Ming  
; ; TITLE OF INVENTION: Cloning, Tissue Distribution, and  
; ; Functional Analysis Of The Human Na+/H+ Exchanger Isoform,  
; ; NUMBER OF SEQUENCES: 12  
; ; CORRESPONDENCE ADDRESS:  
; ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ; ADDRESS: 1300 I Street, N.W., Suite 700  
; ; CITY: Washington  
; ; STATE: D.C.  
; ; COUNTRY: USA  
; ; ZIP: 20005-3315  
; ; COMPUTER READABLE FORM:  
; ; MEDIUM TYPE: Floppy disk  
; ; COMPUTER: IBM PC Compatible  
; ; OPERATING SYSTEM: PC-DOS/MS-DOS  
; ; SOFTWARE: Patentin Release #1.0, Version #1.30  
; ; CURRENT APPLICATION DATA:  
; ; APPLICATION NUMBER: US/09/097,053  
; ; FILING DATE:  
; ; CLASIFICATION:  
; ; PRIORITY APPLICATION DATA:  
; ; APPLICATION NUMBER: US 08/677,734  
; ; FILING DATE: 10-JUL-1996  
; ; ATTORNEY/AGENT INFORMATION:  
; ; NAME: Fordis, Jean B.  
; ; REGISTRATION NUMBER: 32,984  
; ; REFERENCE/DOCKET NUMBER: 05387-0043-00000  
; ; TELECOMMUNICATION INFORMATION:  
; ; TELEPHONE: (202) 408-4000  
; ; TELEFAX: (202) 408-4400  
; ; CURRENT APPLICATION DATA:

Sequence Data						
Query Match		Score	DB	Length		
Best Local Similarity	17.7%	Score	482.5	DB	2	Length 834;
Matches 138; Conservative	31.4%	Pred.	No. 3.6e 38;			
Matches 138; Conservative	88;	Mismatches	158;	Indels	51;	Gaps 17;
SEQUENCE CHARACTERISTICS:						
NAME: Fordis, Jean B.						
REGISTRATION NUMBER: 32,984						
REFERENCE/DOCKET NUMBER: 05387 . 0043 - 00000						
TELECOMMUNICATION INFORMATION:						
TELEPHONE: (202) 408-4000						
TELEFAX: (202) 408-4400						
INFORMATION FOR SEQ_ID NO: 9:						
SEQUENCE CHARACTERISTICS:						
LENGTH: B34 amino acids						
TYPE: amino acid						
STRANDEDNESS: single						
TOPOLOGY: linear						
MOLECULE TYPE: peptide						
RESULT 4 S-08-677-734A-9						
Sequence 10, Application US/08677734A						
Patent No. 5871919						
GENERAL INFORMATION:						
APPLICANT: Brant, Steven R.						
APPLICANT: Yun, Chris C.H.						
APPLICANT: Donowitz, Mark						
APPLICANT: Tse, Chung-Ming						
TITLE OF INVENTION: Cloning, Tissue Distribution, and Functional Analysis Of The Human Na+/H+ Exchanger Iso-						
TITLE OF INVENTION: Function						
TITLE OF INVENTION: NHE3.						
NUMBER OF SEQUENCES: 12						
CORRESPONDENCE ADDRESS:						
ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &						
ADDRESS: Dunner						
SUIT STREET: 1300 I Street, N.W., Suite 700						

CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentent Release #1.0, Version #1.30  
 DURERENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/677,734A  
 FILING DATE: 10-JUL-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fordis, Jean B.  
 REGISTRATION NUMBER: 32,984  
 REFERENCE/DOCKET NUMBER: 05387 0043-00000  
 RELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4000  
 TELEFAX: (202) 408-4400  
 FORMATION FOR SEQ ID NO: 10;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 834 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 677-734A-10

	Identity	Match	Score	DB 1	DB 2	Length	Length	Gaps	Gaps	17;
1	Local Similarity	31.4%	Pred. No.	3.6e-38;	Mismatches	158;	Indels	51;	Indels	
2	Local Similarity	31.36;	Conservative	88;	Mismatches	158;	Indels	51;	Indels	
3	4 8 VNESTITALIIGLCTGIVVILMKGSSHL -	-FVESEDLLFFYLPPITNAFGPKVKKF	105							
4	82 VPESSLIVLGVLGVIV -	-WADHHAASFLPTVVFYFLPPIVTDAGFMPNPKF	136							
5	106 FRNEMTILFGAVMTISFTISTIAIAIFSRMNITGLDV -	-DFLDAIGAFISATDSVCT	163							
6	137 FGNLGTLILYAVGTVWNAAATGGSLYGVPSLQMGDQIGLJLDELFSSLMAAVDPVAV		196							
7	164 LQLVNO-DTFPLFLSIVFGCVVNDATSIKLFNALQNFELV -	-HIDAVVLKLGFNEY	219							
8	197 LAVFEEHVNEVLFILVGEESILNDAVTVVLYNPESFVALGGDNVTGVDCKVGLVSFRV		256							
9	220 LFLSSTFLG -YEAFLSAYIKRLKIGRHSIDREVALMMIMAYLSYMMLABLDLGSILTY		278							
10	257 VSLGGTLVGVVFAPFLS -LTVPR -	-FTKHYRILIEGFVFLISLSYLTSEMSLUSATLAI	312							
11	279 EFGCIVTMWHTHNVTESRVTTHAFATLFSIAETPLFLYVGMDALD1EKWEFASDRPG		338							
12	313 TFCGICCQKYKANTSEQSATTATVRYTMKMLASSAETTIFMELGISAIVNNPIWTW		366							
13	339 KSGISSLLGVLIG -RAAFVFPFLSISNLTKKAPNEKTTWRCQQVWWAGLMRGAVS		396							
14	367 - -NTAFLVLTFLVFEISYRAIGVVLQTVLNRVYQLEPI - -DQVVLSYGGL -RGAVA		419							
15	397 1ALAYNKFRTRSGHTQHGNAI - - -MITSSTTVVLFSTMFV-GMMTKPLTR -LLPASGH		450							
16	420 FALV - - - - -VLLEDKRVKEKNUFVSTTIIWVFVTFQFGTPIKPVQWLKVRSRH		470							
17	451 PVTSEPPSPKSLH 463									
18	471 - - - - -REPRLINEKLH 480									

T 5  
-097-053-9  
Sequence 9, Application US/09097053  
ENT NO. 6392025  
GENERAL INFORMATION:  
APPLICANT: Brant, Steven R.  
APPLICANT: Yun, Chris C.H.

APPLICANT: Donowitz, Mark  
 APPLICANT: Tse, Chung-Ming  
 TITLE OF INVENTION: Cloning, Tissue Distribution, and  
 Functional Analysis Of The Human Na+/H+ Exchanger Isoform,  
 NHE3.  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
 ADDRESSEE: Danner  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/057,053  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/677,734.  
 FILING DATE: 10-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fordis, Jean B.  
 REGISTRATION NUMBER: 32,984  
 REFERENCE/DOCKET NUMBER: 05387.0043-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4000  
 TELEX/FAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 834 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-09-097-053-9

Query Match 17.7%; Score 482.5; DB 4; Length 834;  
 Best Local Similarity 31.4%; Pred. No. 3.6e-38;  
 Matches 136; Conservative 88; Mismatches 158; Gaps 17;

QY 48 VNESTALITLGLCTGVILLMTKGSSHL--FVFSEDLFFYLPPITFNAGFOVKKKOF 105  
 DB 82 VPESALLIVLVLGGIV---WAADHAASFLTLPPTVFFYLPPITVDAFYMPNRLF 136  
 QY 106 FRNFMVITLFGAVGTMISFFTISTIAIAIFSRMNIGTSDVCT 163  
 DB 137 FGNLGTLIYAVGVWNAATGSLYGLSGIMGDLOIQLDFFLFSLMAAVDPYAV 196  
 QY 164 LOVLNQ-DETPFLYSLVFGEGVVNDATSVLFLNALQNFDLY--HIDAAVVLKLGNFYY 219  
 DB 197 LAVEEEHVNEVLFLIVFGESLLNDAVTVLYNFEVYALGGDNVNTGYDCVKGIVSFV 256

QY 220 UFLSSTFLG-VFAGLSSAYIKKKLYGRUSTDREVALMLMAYLSMLAELLDLSGLTV 278  
 DB 257 VSLGGTLVGVFAFLS-LVTR--FTKHVRV1IEPGFVIIPLTVMRQYVWAGLMRGAYS 312  
 QY 279 FFCGTIVMSHYWHNVNTTESSRVTKHAFATLSFIAETFLGVMDALDEKWEFASDRG 338  
 DB 313 TFCGICQCQKYKANI SEQ-SATVRYTMKMAASSSETIIFMFLG-SAVNFITWW---- 366  
 QY 339 KSIGISSIILGLVLIG--RAAFVPLSFLSNLTKKAPNEKITWRQYVWAGLMRGAYS 396  
 DB 367 ---NPAFVLLTFLVSVTRAGVLTWLNRTMVQLEPPI--DQVVLSSYGGL-RGAVY 419  
 QY 397 TALAYNKFRSGHTQLGNAI---MITSTITVVLSTMWF-GMMTKPLIR-LLLPAIGH 450  
 DB 420 FALV-----VLLDDGDKVEKRNLFVSTTLLVVFQVQGLTRIPVQWLKVKRSEH 470

QY 451 PVTSEPPSPKSLH 463  
 DB 471 --REPRLNKEKLH 480

RESULT 6  
 US-09-097-053-10  
 Sequence 10, Application US/09097053  
 Patent No. 6392025  
 GENERAL INFORMATION:  
 APPLICANT: Brant, Steven R.  
 APPLICANT: Yun, Chris C.H.  
 APPLICANT: Donowitz, Mark  
 APPLICANT: Tse, Chung-Ming  
 TITLE OF INVENTION: Cloning, Tissue Distribution, and  
 Functional Analysis Of The Human Na+/H+ Exchanger Isoform,  
 NHE3.  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
 ADDRESSEE: Danner  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/097,053  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/677,734  
 FILING DATE: 10-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fordis, Jean B.  
 REGISTRATION NUMBER: 32,984  
 REFERENCE/DOCKET NUMBER: 05387.0043-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 834 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: peptide  
 US-09-097-053-10

Query Match 17.7%; Score 482.5; DB 4; Length 834;  
 Best Local Similarity 31.4%; Pred. No. 3.6e-38;  
 Matches 136; Conservative 88; Mismatches 158; Gaps 17;

QY 48 VNESTALITLGLCTGVILLMTKGSSHL--FVFSEDLFFYLPPITFNAGFOVKKKOF 105  
 DB 82 VPESALLIVLVLGGIV---WAADHAASFLTLPPTVFFYLPPITVDAFYMPNRLF 136  
 QY 106 FRNFMVITLFGAVGTMISFFTISTIAIAIFSRMNIGTSDVCT 163  
 DB 137 FGNLGTLIYAVGVWNAATGSLYGLSGIMGDLOIQLDFFLFSLMAAVDPYAV 196  
 QY 164 LOVLNQ-DETPFLYSLVFGEGVVNDATSVLFLNALQNFDLY--HIDAAVVLKLGNFYY 219  
 DB 197 LAVEEEHVNEVLFLIVFGESLLNDAVTVLYNFEVYALGGDNVNTGYDCVKGIVSFV 256

QY 220 UFLSSTFLG-VFAGLSSAYIKKKLYGRUSTDREVALMLMAYLSMLAELLDLSGLTV 278  
 DB 257 VSLGGTLVGVFAFLS-LVTR--FTKHVRV1IEPGFVIIPLTVMRQYVWAGLMRGAYS 312  
 QY 279 FFCGTIVMSHYWHNVNTTESSRVTKHAFATLSFIAETFLGVMDALDEKWEFASDRG 338  
 DB 313 TFCGICQCQKYKANI SEQ-SATVRYTMKMAASSSETIIFMFLG-SAVNFITWW---- 366  
 QY 339 KSIGISSIILGLVLIG--RAAFVPLSFLSNLTKKAPNEKITWRQYVWAGLMRGAYS 396  
 DB 367 ---NPAFVLLTFLVSVTRAGVLTWLNRTMVQLEPPI--DQVVLSSYGGL-RGAVY 419  
 QY 397 TALAYNKFRSGHTQLGNAI---MITSTITVVLSTMWF-GMMTKPLIR-LLLPAIGH 450  
 DB 420 FALV-----VLLDDGDKVEKRNLFVSTTLLVVFQVQGLTRIPVQWLKVKRSEH 470

D	257	VSLGGTLLGVVFAFLS -LVTR - -FTKVRVRIIEPGVVFISYLSYLSEMSLSSALLAI	312
Qy	279	FFGIVMSHYTWHNTTESSRVTTKHAFATLSFLAETFLFLYGMDALEIKWEEFASDRPG	338
D	313	TFCGICCCQKYKVNANTSESATVRYTMKMLASSAETLIMFLGISAVANPFTWTW-----	366
Qy	339	KSGISSLGLVLIG - -RAAFVPEPLSPLNSLNUTKAPNEKTIWRQQVVIWAGLMRGAVS	396
D	367	-- NTAFULLTVFISVYRAIGVQLWLNRYRMQLEPI - -DQVVLSTYGL - RAVA	419
Qy	397	IALAYNKFRSGHTQLHGNIA I ---MTISTITVVLFSSTMVF-GMMTKPLIR-LILPASGH	450
D	420	FALV-----VLDGDKVKKEKNLFVSTTIVVFFTIVFOGLTIPLQWLKVKRSEH	470
Qy	451	PVTSEPPSPKSLH 463	
D	471	-- REPRUNEKLH 480	
RESULT 7	US-08-677-734A-11	Sequence 11, Application US/08677734A	
		Patent No. 5,871919	
		GENERAL INFORMATION:	
		APPLICANT: Brant, Steven R.	
		APPLICANT: Yun, Chris C.H.	
		APPLICANT: Donowitz, Mark	
		APPLICANT: Tse, Chung Ming	
		TITLE OF INVENTION: Cloning, Tissue Distribution, and	
		TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,	
		TITLE OF INVENTION: NHE3.	
		NUMBER OF SEQUENCES: 12	
		CORRESPONDENCE ADDRESS:	
		ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &	
		ADDRESS: Dunner	
		STREET: 1300 I Street, N.W., Suite 700	
		CITY: Washington	
		STATE: D.C.	
		COUNTRY: USA	
		ZIP: 20005-3315	
		COMPUTER READABLE FORM:	
		MEDIUM TYPE: Floppy disk	
		COMPUTER: IBM PC compatible	
		OPERATING SYSTEM: PC-DOS/MS-DOS	
		SOFTWARE: Patient Release #1.0, Version #1.30	
		CURRENT APPLICATION DATA:	
		APPLICATION NUMBER: US/08/677,734A	
		FILED DATE: 10-JUL-1996	
		CLASSIFICATION: 435	
		ATTORNEY/AGENT INFORMATION:	
		NAME: Fordis, Jean B.	
		REGISTRATION NUMBER: 32, 984	
		REFERENCE/DOCKET NUMBER: 05387.0043-00000	
		TELECOMMUNICATION INFORMATION:	
		TELEPHONE: (202) 408-4000	
		TELEFAX: (202) 408-4400	
		INFORMATION FOR SEQ ID NO: 11:	
		SEQUENCE CHARACTERISTICS:	
		LENGTH: 831 amino acids	
		TYPE: amino acid	
		STRANDEDNESS: single	
		TOPOLOGY: linear	
		MOLECULE TYPE: peptide	
	US-08-677-734A-11	Query Match 11.7%	Score 480.5; DB 2; Length 831;
		Best Local Similarity 28.6%; Pred. No. 5.7e-38;	
		Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;	
Qy	22	VVSINLFLVALCACIV-LGHLLLEENRWNNESITALLIGCTGVVILLMTKGKSSHL--FV	78
D	54	WAHDIASEF 106	



; TELEFAX: (617) 876-5851  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 635 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-09-014-969-11

Query Match 4.8%; Score 130.5; DB 2; Length 635;  
 Best Local Similarity 19.1%; Pred. No. 0.0041;  
 Matches 118; Conservative 86; Mismatches 206; Indels 209; Gaps 25;

QY 3 MEVAAARUGALYTTSDDA-----SVSINLFLVALCIVACIIGHLJEEENRWVNNESTITALIJI  
 Db 1 MSVGVSHTSAPLSPTSGNSVGNSTFSIMDYYVFVLLVLVSLAIGLYHACRGWGRHVGELL 60

QY 57 IG---LCTGVVILLMTKGKS-----SHLFVESEDFELFI-----YLLPPIENAG 97  
 Db 61 MADRKMCGLPVALSLLATFOAVATLRLPSELYRFQVYFLGILIPANIF---117

QY 98 FOYKKKOFERNFMNTITLEGAVTGMISFTESTIAIAIFSRNIGITLDVGDELAIGAIFSA 157  
 Db 118 -----IPVFRYRHL--TSAYEYLELR--FNK 139

QY 158 TDSVCTLQLNQDETPEFLSYLVFGEGVWNDAATSVLFLHIDAAVFLKFGLNF 217  
 Db 140 TVRVC-----GTVTFIQMVTYMGVLYVAPSIAI-NAVTFQDFD-----175

QY 218 FYFLFSSTFLGVAGLISAYIKKLYIGRHSTDREVALMLMAYLSYMLAEFLDLGILT 277  
 Db 176 --LWLSQLALRVCTVYTAALGGKAVIW---TDVFTLVMFLGOLAVITYSAKVGGLGR 230

QY 278 VFFCGIVMSHYWHNVTPESSRTV-----TKHAFATSFIAETFLFLYVGMDALDIE 328  
 Db 231 V-----WAVASOGRISGFELDPDPFVRHTFWTLAFCGGYFMMMSLYGVNQAOQW 279

QY 329 KWEFASDRPGKSIGIS-----SILGLVLIG-----RAAFVFP 361  
 Db 280 R--YLSSSETKAVALSCYAVFPFQQVSLCVGLIGLYMAYQEFPMISOQAQAPDQFV 337

QY 362 LSFSLNLTKKAPNEKTIWQRQVYIWINAGLMRGAVS-TALAYNKFTRSGHQTL-----412  
 Db 338 LYPMVMDLKGLPG-----LPGLFLTACLFSSLSTSISAFNSLATVTMEDILRPWFPEF 390

QY 413 -HGNAIMTSTTP-----VVLFLSTMVFGMMTTPKLIRLLPASGHPV 452  
 Db 391 SEARAIMLRSRGLAFGYGILGLCUGMAYISSQMGVFLVQAAISTEGMGVGSPLGFLCLGMFFPC 450

QY 453 TSBPSSPSLHSPL-----LTSM-----QSDSLSPSTN--TVRPLLRLM 490  
 Db 451 ANPGAVVGLLAGLVMARWIGIGSIVTSMGFMSMPPSPNSSSFLPTNLTVATVTLMLPL 510

QY 491 LT--KPT-----HTVHYYW 502  
 Db 511 TTSKPKTQIQRFLPSYIWM 529

RESULT 11  
 US-09-134-001C-4425  
 ; Sequence 4425, Application US/09134.001C  
 ; Patent No. 6380370  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
 ; FILE REFERENCE: GTC-007  
 ; CURRENT FILING DATE: 1998-08-13  
 ; PRIORITY APPLICATION NUMBER: US/09/134,001C  
 ; PRIOR APPLICATION NUMBER: US 60/064,964  
 ; PRIOR FILING DATE: 1997-11-08  
 ; PRIORITY APPLICATION NUMBER: US 60/055,779  
 ; SEQ ID NO 5655  
 ; LENGTH: 600  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus epidermidis  
 US-09-134-001C-5655

Query Match 4.6%; Score 124.5; DB 4; Length 605;  
 Best Local Similarity 22.9%; Pred. No. 0.0015;  
 Matches 105; Conservative 69; Mismatches 190; Indels 97; Gaps 24;

QY 22 VVSINLFLVALCIVACIIGHLJEEENRWVNNESTITALIJIIGLCTGVVILMFKGSSSHLYFVSE 81  
 Db 18 MLTIVLFLAI-----SFSQWLASRKPSTIVWAFLGVLGFLPGLKPEALGPFAEFS 73

QY 82 DLFFFYLLPPIENAGFOVKKOPFRNMFTITLEGAVTGMISFTIS-----IAIAIAFL 135  
 Db 74 ---IVSLAVAITL--FEGSSNLDRE---LKGISKAVIRLITIGAGIAWLGIAIH 122

QY 136 SRMNIGTLDVGFDFLAIAGAIFSATSVCTLQLVNQDETFLYSLVFGEGVNDATS-TVL 193  
 Db 123 VTMMN-PLSIS--FVIGGLEPLITGPTVIOPLIKAKVKNVDSYLWRWSIILDPIGPIA 179

QY 194 FNALONEDLVHTDAAVFLKFLGNFFYFLFSLSTFLGVFAGLSSAVIKKLYIGRHSTDREV 253  
 Db 180 LTAFYVFLQFOFLFEEGIGLVLVIL--FLKLUAAILFLGGAFLFNLWIL-----SQDKIP 229

QY 254 ALMMIMAYLSYMLA-----ELLDLISLTYVFFCGIVMSHYWHNVTPESSRTVKHAFAT 307  
 Db 230 QSLMPPIOLVFLILTFSCIDBTLSFSGLLAVTIGLMMARKKRIDLIFKE--SDHFIDN 286

QY 308 LSFIATEFLFLYGMID-----ALDIKEWFAASDRPGKSIGISSILGLVLIGRAAFVPL 362  
 Db 287 ASSILVSTVFLITSSLTKDVLLNWLSWQL-----ILFSLVMI--VLRVPI 330

QY 363 S-FLSNLTKKAPNEKTIWQRQVYIWINAGLMRGAVS-TALAYNKFTRSGHQTLHGNAFM- 418  
 Db 331 SVLLSPL-----GTEETKKKRAVV--ALMAPRQVYIWINAGLMRGAVS-TALAYNKFTRSGHQTLHGNAFM- 418  
 Db 373 DKIPMAQYTPVTFGLVETVVIIGFGFTPLSKLFGVASTEP 414

RESULT 12  
 US-09-134-001C-5655  
 ; Sequence 5655, Application US/09134.001C  
 ; Patent No. 6380370  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
 ; FILE REFERENCE: GTC-007  
 ; CURRENT APPLICATION NUMBER: US/09/134,001C  
 ; PRIORITY APPLICATION NUMBER: 1998-08-13  
 ; PRIORITY APPLICATION NUMBER: US 60/064,964  
 ; SEQ ID NO 5655  
 ; LENGTH: 600  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus epidermidis  
 US-09-134-001C-5655

Query Match 4.4%; Score 118.5; DB 4; Length 800;  
 Best Local Similarity 21.3%; Pred. No. 0.0085;  
 Matches 101; Conservative 71; Mismatches 173; Indels 129; Gaps 22;

QY 57 IGLCTGVVILMFKGSSSHLYFVSEDL--FVIYLLPPIIFNAGFQVKKQFPRFNM 110



RESULT 15  
US-08-800-291B-4

Sequence 4, Application US/08800291B  
Patent No. 6153140

GENERAL INFORMATION:

APPLICANT: J.D. Young & C.E. Cass  
TITLE OF INVENTION: cDNA ENCODING NUCLEOSIDE TRANSPORTER  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,291B  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/499,314  
FILING DATE: 7-JULY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07254/044WO1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 650 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-800-291B-4

Query Match Score 111; DB 4; Length 650;  
Best Local Similarity 21.3%; Pred. No. 0.034;  
Matches 98; Conservative 51; Mismatches 174; Indels 138; Gaps 19;

Qy 21 SVVSNFLVALLCAC- Score 111; DB 4; Length 650;  
Qy 22 SVVSNFLVALLCAC- Score 111; DB 4; Length 650;  
Db 182 SFAGICVFVALLFACSKHCAVSRAVSNGLGLOFVLGLVIRTEPGFIAFEMIGEQLR- 240  
Qy 55 LIIGLCTGVVLLMTKGSSHLFVSE- Score 111; DB 4; Length 650;  
Db 241 -----IFLSYTKAGSS- Score 111; DB 4; Length 650;  
Qy 111 TITLFGAVGTMISSFTTISIAIAFSRMNIGTLVDGLAIGAFSATDSVCTLQVNQD 170

Db 277 VISVLYHGLM- - - QWYLKLAWLMOVTMGITPATETLSVAGNF- - - - - VSQT 321  
Qy 171 ETPFL- - - - - YSLVFGE- - - - - GVNDATSVLFNALQNFLD 202  
Db 322 EAPLILRPLADMTLSEYHVVMGGATAGSLLGAYISFGI- - - - - DATLIAASVM 374  
Qy 203 VHIDAAVLKFLGNFNFYFLFSSTFLGVFAGLSSAYIJKLYGRHSTREVALMM- - - - - 257  
Db 375 - - - - - LMAYLSYM- - - - - LAELLDLSGLTVFFCGIV- - - - - MSHTWHNVTESSRT 300  
Qy 258 - - - - - APCALIALSKVYPVEEESFRREEGVKLTYGDANLIEASTGAAISVKVWANIA 430  
Db 431 ANLIAFLAVLDFINAWSLWGLMDYIOGLSFQLICSYILRPVAFMLGVAWEDCPVVAELL 490  
Qy 301 TKHAATLSEIATFLFLVYGMDALDIKEWFAASDRPGKSIGTSSILGLVIGRAAFV 360  
Db 491 GTKLFLN- EPVAYQDLSKYKORRLAGAEEW- VGDRKQWISVRAEVLTTFATQGEANESS 547  
Qy 361 PLSEFLNLTKKAPBKRTQRQQVTTWAGLMLRGA- VSTALA 400  
Db 548 IGIMUGGLTSMVWORKSDFSQTVL- - - RALFTGACVSLVNA 585

Search completed: March 26, 2003, 18:54:54  
Job time : 34 secs



20	184.5	6.8	686	10	US-09-815-242-5777	
	21	184.5	6.8	692	10	US-09-815-242-12734
	22	153.5	5.6	516	9	US-09-738-626-5086
	23	133	4.9	129	9	US-09-925-299-1210
	24	133	4.9	129	10	US-09-925-299-2110
	25	116.5	4.3	480	9	US-09-895-919A-92
	26	110.5	4.1	450	10	US-07-741-669-385
	27	109.5	4.0	296	10	US-09-815-242-5098
	28	108	4.0	539	10	US-09-815-242-5139
	29	105.5	3.9	461	10	US-09-815-242-12175
	30	105.5	3.9	490	9	US-09-738-626-5981
	31	105	3.9	422	10	US-09-815-242-5682
	32	105	3.9	458	9	US-09-738-626-5686
	33	104	3.8	444	9	US-09-738-626-5577
	34	104	3.8	816	9	US-09-815-242-588-5
	35	103.5	3.8	388	10	US-09-815-242-1458
	36	103.5	3.8	388	10	US-09-881-752A-350
	37	102	3.7	494	12	US-10-033-109-6
	38	99.5	3.7	717	9	US-09-883-434A-5
	39	99.5	3.7	1042	10	US-09-888-615-74
	40	99	3.6	371	9	US-09-759-103B-881
	41	99	3.6	525	9	US-09-882-694-8
	42	99	3.6	962	9	US-09-738-626-3800
	43	99	3.6	1116	9	US-09-835-916B-12
	44	97	3.6	497	10	US-09-734-676-6
	45	97	3.6	807	10	US-09-895-686-6

ALIGNMENTS

The total s

Query	Score	Match	Length	DB	ID	Description	
						No.	result
1	2082	76.5	546	9	US-10-155-535-2	Sequence 2, Appli	
2	2023.5	74.3	538	9	US-09-834-998A-1	Sequence 1, Appli	
3	1931	70.9	552	9	US-10-155-535-4	Sequence 4, Appli	
4	561	20.6	521	9	US-10-155-535-6	Sequence 6, Appli	
5	545.5	20.0	446	9	US-10-217-096-4	Sequence 4, Appli	
6	541.5	19.9	509	10	US-09-800-729-93	Sequence 93, APP	
7	541.5	19.9	526	10	US-09-800-729-180	Sequence 180, APP	
8	539	19.8	645	9	US-10-217-096-2	Sequence 2, Appli	
9	538	19.8	669	9	US-09-834-998A-2	Sequence 2, Appli	
10	533	19.6	633	9	US-09-834-998A-3	Sequence 3, Appli	
11	485	17.8	896	9	US-10-217-096-6	Sequence 6, Appli	
12	478	17.6	822	10	US-09-824-734-3	Sequence 3, Appli	
13	314	11.5	370	10	US-09-800-729-215	Sequence 215', AP	
14	292.5	10.7	339	10	US-09-800-729-128	Sequence 128, AP	
15	292.5	10.7	339	10	US-09-800-729-129	Sequence 129, AP	
16	285.5	10.5	1146	10	US-09-824-734-2	Sequence 2, Appli	
17	231.5	8.5	684	10	US-09-815-21-10712	Sequence 4, 10712,	
18	210	7.7	424	10	US-09-824-734-4	Sequence 5, Appli	
19	192	7.1	94	9	US-10-217-096-5	Sequence 5, Appli	

Qy 195 NALONFDLVHIDAAVVLKFLGNFFYLFLSSTFLGVFAGLLSAYIILKKLYIGRHSTDREVA 254  
 Db 195 NATOSFDLTHLNHEAFAQFGNPFYFLSTGUGATGLISAVVKKLYGRUSTDREVA 254  
 Qy 255 LMMLMAYLSYMLAELLDLSGLTIVFFCGLVMSHTWHNTESSRVTTKHAFATLSFLAET 314  
 Db 255 LMMLMAYLSYMLAELFLAFLSGLTLVFFCGLVMSHTWHNTESSRITTKHAFATLSFLAET 314  
 Qy 315 FFLFLVGMDALDTEKEWFAASDRGKSGITSILLGLVIGRAAFVPLSFLSNLKTPN 374  
 Db 315 FFLFLVGMDALDTEKEWFAASDRGKSGITSILLGLVIGRAAFVPLSFLSNLKTPN 374  
 Qy 375 EKTIWROQVVIWAGLMRGAVSIALTOLNKFTRSGHTOLHGNAIMTSTTIVNLFSFTMVF 434  
 Db 375 EKTIWROQVVIWAGLMRGAVSIALTOLNKFTRSGHTOLHGNAIMTSTTIVNLFSFTMVF 434  
 Qy 435 MMTPKLPLRLLP----ASGHPTVSEPPSPSKLHSPLITSMQGSDLE--STINIVPSS 486  
 Db 435 MMTPKLPLRLLP----ASGHPTVSEPPSPSKLHSPLITSMQGSDLE--STINIVPSS 486  
 Qy 487 LRMLLTKPTHTVHYWWRKFDALMRPMGGFGRGPFPFSPGSPTEQS 531  
 Db 495 LRGFLMRPRTTVHYWWQDFDAFMRPVFGGRGPFPFVPGSPTERS 539

RESULT 2  
 ; Sequence 1, Application US/09834998A  
 ; Patent No. US20020178464A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaxiola, Roberto A.  
 ; ATTORNEY: Flink, Gerald R.  
 ; TITLE OF INVENTION: Proton Transporters And Uses In Plants  
 ; FILE REFERENCE: 0319-2004-002  
 ; CURRENT APPLICATION NUMBER: US/09/834,998A  
 ; CURRENT FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: US 09/644,039  
 ; PRIOR FILING DATE: 2000-08-22  
 ; PRIOR APPLICATION NUMBER: US 09/644,808  
 ; PRIOR FILING DATE: 1999-11-10  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO: 1  
 ; LENGTH: 538  
 ; TYPE: PPT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Arabidopsis - AtNhx1

US-09-834-998A-1

Query Match 74.3%; Score 2023.5; DB 9; Length 538;  
 Best Local Similarity 73.3%; Pred. No. 1.1e-169; Indels 3; Gaps 2;

Matches 389; Conservative 60; Mismatches 79; Indels 3; Gaps 2;

3 NEVAARLGLAYTSDYASVSVSINLFLVALCAVGHLEENPKVNESTITALIGLC 62  
 2 IDSLSLVRKPLPSL-STDSHASYVNAFLVALCAVGHLEENPKVNESTITALIGLC 62

Qy 63 VVLLMTKGKSHLFVPSEDLFYIYLPLPFLNAGQVKKKQFFRNEMTILFGAVGTII 122  
 Db 61 VVLLMTKGKSHLFVPSEDLFYIYLPLPFLNAGQVKKKQFFRNEMTILFGAVGTII 120  
 Qy 123 SEFTISIAAIAIFSRMNGTUDGDFLAIAGAIFSATDSVCLQLNQDETPFLYSLVGE 182  
 Db 121 SCTIISLGVTQFFKKLDIGFLDGYLAIAGAIFSATDSVCLQLNQDETPFLYSLVGE 180  
 Qy 183 GVNDNTSIVFLNALONFLVHIDAAVVLKFLGNFYLFLSTFLGVFAGLLSAYIKKL 242  
 Db 181 GVNDNTSIVFLNALONFLVHIDAAVVLKFLGNFYLFLSTFLGVFAGLLSAYIKKL 240  
 Qy 243 YIGRHSTDREVALMMMLMAYLSYMLAELLDLSGLTIVFFCGLVMSHTWHNTESSRVT 302

Db 241 YGFRHSTDREVALMMMLMAYLSYMLAELLDLSGLTIVFFCGLVMSHTWHNTESSRVT 300  
 Qy 301 TKHAFATLSEFAETELFLYGMDALDTEKEWFAASDRGKSGITSILLGLVIGRAAFVFL 360  
 Db 302 TKHAFATLSEFAETELFLYGMDALDTEKEWFAASDRGKSGITSILLGLVIGRAAFVFL 361

RESULT 3  
 US-10-155-535-4  
 ; Sequence 4, Application US/10115535  
 ; Publication No. US2003046729A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blumwald, Eduardo  
 ; ATTORNEY: Apse, Mari S  
 ; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY  
 ; EXPRESSION OF VACUOLAR CATION PROTON ANTIPORTERS  
 ; FILE REFERENCE: 529152007/20  
 ; CURRENT APPLICATION NUMBER: US/10/155,535  
 ; CURRENT FILING DATE: 2002-05-24  
 ; PRIOR APPLICATION NUMBER: 09/271,584  
 ; PRIOR FILING DATE: 1999-03-18  
 ; PRIOR APPLICATION NUMBER: 60/078,474  
 ; PRIOR FILING DATE: 1998-03-18  
 ; PRIOR APPLICATION NUMBER: 60/116,111  
 ; PRIOR FILING DATE: 1999-01-15  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO: 4  
 ; LENGTH: 552  
 ; TYPE: PPT  
 ; ORGANISM: Arabidopsis thaliana

US-10-155-535-4

Query Match 70.9%; Score 1931; DB 9; Length 552;  
 Best Local Similarity 69.6%; Pred. No. 1.5e-161; Mismatches 78; Indels 20; Gaps 4;

Matches 377; Conservative 67; Mismatches 78; Indels 20; Gaps 4;

1 MGMEVAARLGLAYTSDYASVSVSINLFLVALCAVGHLEENPKVNESTITALIGLC 60  
 Db 3 IGLSTMKEATLPE-ADHASVVSNNFLVALCAVGHLEENPKVNESTITALIGLC 61  
 Qy 61 TGVVLLMTKGKSHLFVPSEDLFYIYLPLPFLNAGQVKKKQFFRNEMTILFGAVGT 120  
 Db 62 TGVVLLMTKGKSHLFVPSEDLFYIYLPLPFLNAGQVKKKQFFRNEMTILFGAVGT 121  
 Qy 121 MISFTTISIAAIAIFSRMNGTUDGDFLAIAGAIFSATDSVCLQLNQDETPFLYSLV 180  
 Db 122 LISFVLSGAKHLFEKMNIGDTIADYLAIGAIFSATDSVCLQLNQDETPFLYSLV 181  
 Qy 181 GEGVNDNTSIVFLNALONFLVHIDAAVVLKFLGNFYLFLSTFLGVFAGLLSAYIK 240  
 Db 182 GEGVNDNTSIVFLNALONFLVHIDAAVVLKFLGNFYLFLSTFLGVFAGLLSAYIK 241  
 Qy 241 KLYIGRHSTDREVALMMMLMAYLSYMLAELLDLSGLTIVFFCGLVMSHTWHNTESSRVT 300  
 Db 242 KLYIGRHSTDREVALMMMLMAYLSYMLAELLDLSGLTIVFFCGLVMSHTWHNTESSRVT 301  
 Qy 301 TKHAFATLSEFAETELFLYGMDALDTEKEWFAASDRGKSGITSILLGLVIGRAAFVFL 360  
 Db 302 TKHAFATLSEFAETELFLYGMDALDTEKEWFAASDRGKSGITSILLGLVIGRAAFVFL 361

Qy 361 PLSFLSNTKKAPNEKITWQQVYIWAGLRAVSIALAYNKFRSGHTQLHGNATMT 4.20  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 362 PLSFLSNTKKAPNEKITWQQVYIWAGLRAVSIALAYNOPTSGTIVKGNATMT 4.21  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 421 STIVVLFSTIVFGMMTKPLJIRLLPASCHPVTS-----EPSSPKSLHSPLITS 4.69  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 422 STIVVLFSTIVFGMMTKPLJIRLLPASCHPVTS-----ILHEPLIST 4.77  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 470 MGSDELSTINIVRPSLMLTPTKTHWYWRKFDDALMRPMFGGRFVSPSPGSPTE 5.29  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 478 QGQESEDEPEQHV----SFREWKSPSPRSATHYWRKFDDNAVMRRLFFGRSVSPVPGSPTE 5.33  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 530 QS 5.31  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 534 NS 5.35  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  


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**RESULT 4**  
 US-10-155-535-6  
 ; Sequence 6, Application US/10155535  
 ; Publication No. US2003046729A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blumwald, Eduard  
 ; APPLICANT: Apse, Marius  
 ; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY  
 ; EXPRESSION OF VACUOLAR CATION-PROTON ANTIPORTERS  
 ; FILE REFERENCE: 52912000720  
 ; CURRENT APPLICATION NUMBER: US/10/155,535  
 ; CURRENT FILING DATE: 2002-05-24  
 ; PRIOR APPLICATION NUMBER: 09/271,584  
 ; PRIOR FILING DATE: 1999-03-18  
 ; PRIOR APPLICATION NUMBER: 60/078,474  
 ; PRIOR FILING DATE: 1998-03-18  
 ; PRIOR APPLICATION NUMBER: 60/116,111  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 6  
 ; LENGTH: 521  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-10-155-535-6

Query Match 20.6%; Score 561; DB 9; Length 521;  
 Best Local Similarity 32.5%; Pred. No. 3\_1e-4; Mismatches 205; Indels 68; Gaps 22;

Matches 173; Conservative 86; Mismatches 205; Indels 68; Gaps 22;

Qy 20 ASVSYNIFVALCIVLGHLLEENR-WVNESTITALIIGLCTGYVILLM-TKGKSSH 76  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 22 AAGVGLLQIMMLVLSPFLGHYLRRHRYLPPEASGSLLIGLVGIANISDTETSIRTW 81  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 77 FVSEDFLFIYLPLPFINAGFOVKQQFRNFMITLEFGAVGTMISFTISIAATFS 13.6  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 82 FNPHEEFFFLPPIQFQSGESLQPKMFNSFNGATVFAITGTF----VASVTTGG 13.4  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 137 RMNTG-----TLDVGFELGAIFMSNTDSVCTLQVQNQDETTP-LYSVFGGVVND 188  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 135 LVIIGGSMYLMYKLFPVCLMFGALISATDPVTLVSLFQDYGTDVNLVLYVFGESVINDA 194  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 189 TSIVLFNAL----QNFDLVHTDAAVYLKFGLNNFFYLFLSSSTFLGVAGLSSAYIKKLY 24.3  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 195 MATSLYRMTSLVNQSSSGEHHFMVVI----RFFETTAGSMSAGVGFTSALLFK-Y 24.7  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 244 TG---RHSDIREVALLMMAMSYMLAELLDLSGLITVFCGIVMSHYTWHTTESSRV 300  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 248 AGLDTENLQNLCLECPFLVPPYFSMVAEGVGLSGSIVLFTGIVMKYTFMSLSEASQSF 307  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 301 TKHAFATSLFIAETPLFLVYGM-ALDEKWEFASDRGKSIGISSTLLGLVLIG-RAA 357  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 308 VSSFPHLSSLAAEFTFYMGFDIAQEHWSH-----VGFILSILFIGVARAV 357  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 358 FVFPLSLSNLTKKAPNEKITWROQVVVWAGLMRGAVSIALAYNKF-TRGHTQLHGN 4.15  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

**RESULT 5**  
 US-10-217-096-4  
 ; Sequence 4, Application US/10217096  
 ; Publication No. US2003044933A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Rory A.J.; Ferriera, Holly M.  
 ; TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger  
 ; FAMILY MEMBER AND USES THEREOF  
 ; FILE REFERENCE: MPI01-14791RM  
 ; CURRENT APPLICATION NUMBER: US/10/217,096  
 ; CURRENT FILING DATE: 2002-08-12  
 ; PRIOR APPLICATION NUMBER: 60/312,544  
 ; PRIORITY FILING DATE: 2001-08-15  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 4  
 ; LENGTH: 446  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Consensus  
 ; US-10-217-096-4

Query Match 20.0%; Score 545.5; DB 9; Length 446;  
 Best Local Similarity 34.2%; Pred. No. 5.8e-40;  
 Matches 157; Conservative 79; Mismatches 162; Indels 61; Gaps 15;

Qy 27 LFVALUCACTVLGHLEE-NRWVNNESTITALIIGLCTGYVILLMTRGKSSHFLFVSEDFLFF 85  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 4 LIIILVLAKTLAHFKRLGKAIPPSLMLLAGLGLGPGL-----GLIVLSEVFF 55  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 86 IYLLPEPLIENAGFOVKKKOPFERNFPTITLEFGAVTMISFTISTIAIAFISRMNG----141  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 56 EILPLPTEFLFEAGLEDLRELFRNLSLILLAVLGLSILASVIGGLYALVPLFGQOLV 115  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 142 TLVDGFELAIGAIFSATDSVCTLQVLNQDE----TPEFLYSLVEGEVNVNDATSVLFNAL 197  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 116 DDLAAALLPSATLSATDPAVLAKFGELKRYNKLGLTFLFSESSLNDAVVLLAVL 175  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 198 QNF-----DLVHIDAVVLFRLPNFNPFYLFLSFLSTFLGVAG-----LLSAYITKKLY 244  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 176 ISFAQGDNSEAVEAFDIFGVLSFL----VVFFGLLIGLVLGPFLS-----LI 224  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 245 GRHSTDPR-----EVAMMLMAYLTYMLAEFLDLSGLTUVFLFGVMSH-YTWHNVTE 295  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 225 TRFDDEGPLEPLDRLTEPLVLLAVLAYLIAEMGLGSILAVFAGLASNAYVANISE 284  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 296 SSRVTKHFATLSELTAEFLFLYGC-MDALDIKEWFAFSDRPGKSIGTSIILGLV-----351  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 285 KSRRTKYEWKMLSFPEPLFVLGLSLLDSLVSUHNWANTEDL-BESTVIAFLILAVAI 343  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 352 LIGRAAEVFPLSLSNLTKKAPNEKITWROQVVVWAGLMRGAVSIALAYNKF-405  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 344 LLARAGVFLLTLLNFFERKRSNEWSEHTFROLVWGGFLURGAVALALASGPLT 403  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 406 RSGHTOLHGNAIMITSTPITVVLFLSTMVFGHMKTPLKIRL 444  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 404 LEDTSGSPARDLILITTAIVVVLVTVLQGITLKPLVYKL 442  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 RESULT 6  
 US-09-800-729-93

Sequence 9<sup>3</sup>, Application US/09800729  
 Patent No. US20020068319A1  
 GENERAL INFORMATION:  
 APPLICANT: Ni et al.  
 TITLE OF INVENTION: 32 Human secreted proteins  
 FILE REFERENCE: PZ044P1  
 CURRENT APPLICATION NUMBER: US/09/800,729  
 CURRENT FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: PCT/US00/26013  
 PRIOR FILING DATE: 2000-09-22  
 PRIOR APPLICATION NUMBER: 60/155,709  
 NUMBER OF SEQ ID NOS: 217  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 93  
 LENGTH: 509  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: SITE  
 NAME/KEY: SITE  
 LOCATION: (20)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (168)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (198)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (168)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (20)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (198)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (199)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (244)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (246)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (294)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (301)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (303)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (493)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (498)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (499)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (505)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-09-800-729-93

Query Match 19.9%; Score 541.5; DB 1.0; Length 509;  
 Best Local Similarity 30.8%; Pred. No. 1.5e-39; Mismatches 81; Indels 81; Gaps 14;

By 23 VSINLFWALLCAGTCVGHLLNEEN--RWNNESTITALTIGLCGVILL--MTRGKSSHL- 76  
 Db 19 VXLTFILLTITLTIWLRHRRVRLHETLAMIGLIVGLRGTATSGDKSLS 78  
 By 77 --- -FVSESDLPFIYLLPPI 92  
 Db 79 CTDQEDRAFSTLLNVSGKFFEYTLKGEISPGBKNSEQNDMLRKVTEDPVEFNILLPPI 138

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 LOCATION: (216)  
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (37)  
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (115)  
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (215)  
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (263)  
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (311)  
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (318)  
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids



;

FEATURE:  
; OTHER INFORMATION: Human - hsNhe-6  
US-09-834-998A-2

Query Match 19.8%; Score 538; DB 9; Length 669;  
Best Local Similarity 29.9%; Pred. No. 4.8e-39;  
Matches 164; Conservative 97; Mismatches 210; Indels 78; Gaps 18;

QY 1 MGMEVAARLGALEYTSDAYSVSINLEVALLCACIVLGHLLDEN - -RWNVESITALLIG 58  
Db 53 MDEEIVSEKQAEEFSHRSANLL--IFLILLTLLTITIWFKHRRAREFLHETGLAMIY 109  
QY 59 LCTGVV - - - - -ILLMTKGSSH --LFVSEDLFFYLPLPPIENAGFOVKK 102  
Db 110 LLVGLVLHYGIVHPVDYNNVTISCEVOSSPPLLVDPEFFNLLPPIFYAGYSLKR 169  
QY 103 KOFFRNFMFTTGFAYGTMISFFTISIAIAFESRMNIGTLDVGDF - - -LAIGAIFSA 157  
Db 170 RHFFRNLGSILAYAFLTAISFVIGSIMYGTLMKVTCGLAGDFYFTDCCLFGALVSA 229  
QY 158 TDSVCTLQLNQDETPE-LYSVFGCVNDAATSIVLNALQNF - - -DLVH- IDAAVL 211  
Db 230 TDPVTVALAFHQLQDVELYALFGESVNDAIVLSSVAYQPGDNHSTEDVTA 289  
QY 212 KELGNFPYLPFSSTFVQFAGLMLSYMLMAEL 269  
Db 290 RSIGIFGIFSGSFANGAATGVTALEYTNLSTESQHRTKQLELLA 346  
QY 270 LDLSGLTVEFCIVSHYTHWNTESSRTVKHATPLSTIAETFLFLYGMDALDIEK 329  
Db 347 WGETGVAVLVECGITOAHYTNLNLSTESQHRTKQLELLA 406  
QY 330 WEFASDRPGKSIGGISSLLGLIGRAAFVPLSFLSNLTKAPNEKITWQOQVVIWAG 389  
Db 407 HVF -- NPTFVG -- -AFV/FIFLGRANNYPLSLUNLGRS -- KIGSNEQHNMFMAG 456  
QY 390 LMRGAVSIALAYNKFTRSGHTQHGNAIMITSTIVLFLSTMFGMMTKPLLIRLLLPSG 449  
Db 457 L -RGAMAFALAR -- -DIATYARQMMPSSTLLIVEFTWVFGGGTTAMLSCL - - - 504  
QY 450 HPTVSEPPSPSLHSPLTSQMSDLESTNIVRSSRLMLLTKEPTVHYYWRKFDDAL 509  
Db 505 HIRVGVDSDOHHLGVP - - - - ENERRTKAESAWLFRM - - - - -WYNFDHNY 545  
QY 510 MRPMERGGRG 518  
Db 546 LKPPLTHSG 554

RESULT 11  
US-10-217-096-6  
; Sequence 6, Application US/10217096  
; Publication No. US20030044933A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J., Ferriera, Holly M.  
; TITLE OF INVENTION: 96895, A Human Sodium Hydrogen Exchanger  
; TITLE OF INVENTION: Family Member and Uses Therefor  
; FILE REFERENCE: MP10-147P1RM  
; CURRENT APPLICATION NUMBER: US/10/217,096  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: 60/312,544  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 896  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-217-096-6

Query Match 17.8%; Score 485; DB 9; Length 896;  
Best Local Similarity 29.9%; pred. No. 3e-34;  
Matches 155; Conservative 93; Mismatches 190; Indels 80; Gaps 22;

QY 22 VVSINLFLVALCACIVLGHLEE - NRWNVESITALLIGCTGVVILLMTKGSSHLFVFS 80

Db	49 LVALWILVIASTIAK--IVFLHSRSKVTSLVPESCCLLILLGLVGGIVLVAYAKAYQL---E 103	Db	215 VCLVGGEQINNIGLLDTLLFGSIISAVDPVAVVAVFEEIHINELLHLVFGESLLNDAVT 274
Qy	81 EDLFFFYLLPPLIFENAGFQVKKKOFFERNFMITITLEFGAVCTMISFETISSA-----AIAI 134	Qy	191 IVLENALO--NEDLWHVHDAVVLKPLGNNFFLFLESSLTFLGFAGLISAYIKKLIGRH 247
Db	104 PGTFFLFLPPIVLDGSYFQPSRLRFLDNIGAILTYAVVGTFLWNAAFTTGALMGLQAGIL 163	Db	275 VVLYHFFEFANDSISGI--SDIFLGFEL-SFYVVALGGVFVGYVTAFTSR--FTSH 329
Qy	135 FSRMRNIGTLDVGDFLAIGAFSAATDSVCLQLQVNLNQ--DETPFLPSLYVGEGVVNDATSI 191	Qy	248 STDREVALMLMLMAYLSYMAELLDLSGLTIVLVEPCGIVMSHTYTHWNTESSRVTTKHFAT 307
Qy	152 APRVQAGL--DLVFLQNF--DLVFLQNF--DLVFLQNF--DLVFLQNF--DLVFLQNF--DLVFLQNF 218	Qy	303 IRVIEPLEVELYSMAYLSAELLSLGLLIGLIGRAAFVPMPLSFLS 366
Db	164 APRVQAGL--DLVFLQNF--DLVFLQNF--DLVFLQNF--DLVFLQNF--DLVFLQNF--DLVFLQNF 218	Db	330 LSFIATEFLFLYGMAL-DIEKWFASDRPGKSIGISSILUGLVLIGRAAFVPMPLSFLS 366
Qy	192 VFLNALQNF--DLVFLQNF--DLVFLQNF--DLVFLQNF--DLVFLQNF--DLVFLQNF--DLVFLQNF 245	Qy	308 WSSSETLFLIFLGVSTVAGSHOWNW----TVFISTLL--FCCLARVQLVLTWFI 440
Db	219 VLYKVCNSFVEMGSANVQATDYLGKVASLFLVSGGAAGVGLVFAFLALTTRFTKVRKI- 277	Qy	367 NFKAPNEKITWQOQVVIWAGLARGVASYIALAKYKFRSGHTQHGNIAIMTSITVVY 426
Qy	246 RHSTDREVALMLMLMAYLSYMAELLDLSGLTIVLVEPCGIVMSHTYTHWNTESSRVTTKHF 305	Db	441 N--KERTVKLTPDQFTIAYGGL--RGATAFSIGY--LMDKXHEPMD--LFLTAITVI 492
Db	278 --LEPLLNFLLAYAALTAEMASLTLAVTMCGLCKKYVEANISHKSRSRTVKTDM 332	Qy	427 LFSTMVFGMMTKPLIRLILLPLPASHPTSEPPSPSKLSHSPLTSMOGSDELSTTNIVRPSS 486
Qy	306 ATLSFIAETFLFLYGMAL-DIEKWFASDRPGKSIGISSILUGLVLIGRAAFVPMPL 362	Db	493 EFTVFOQGMNTIRPLDLL----AVKVKQETRSINPEIHTQFLDHLTGIEDIC--- 542
Qy	333 KTLASCAETVFMGLISAVDSSKNAWD-----SELVLTGLLFLFRAFLGVVLIQ 382	Qy	487 LRMLLTKPHTVHIVYWKEDDALMR 511
Db	363 SFLSNLTKAPNEKITWQOQVVIWAGLARGVASYIALAKYKFRSGHTQHGNIAIMTS 422	Db	543 -----GHYGHHHWK--DKLNR 556
Qy	383 TWLNQFLRFLVPLDKI--DQVMSYGGL-RGAVAFALV---ILLDRTRVPAKDYFATT 434		
Qy	423 ITVVLPSTMFQGMMTKPLIR-LLLPASGHPTSEPPSPSKLSHSPLTSMOGSDELSTTNI 481		RESULT 13
Db	435 IIVVFFTVVQGLTIPKLVKUKVURKREH--HKTTLNQEULHEHTFDHI---LAAVEDY 487		US-0-800-729-215
Qy	482 VRPSSLRMLLTQKTPHTVHIVY--WRFKD---DALMR 511		Sequence 215, Application US/09800729
Db	488 V-----GHGHGHYHWDRWEQDKKYLSQLMR 514		Patent No. US20020068119A1
			GENERAL INFORMATION:
			APPLICANT: Ni et al.
			TITLE OF INVENTION: 32 Human secreted proteins
			FILE REFERENCE: PZ04/P1
			CURRENT APPLICATION NUMBER: US/09/800,729
			PRIOR APPLICATION NUMBER: 2001-03-08
			CURRENT FILING DATE: 2001-03-08
			PRIOR FILING DATE: 1999-09-24
			NUMBER OF SEQ ID NOS: 217
			SOFTWARE: PatentIn Ver. 2.0
			SEQ ID NO: 215
			LENGTH: 370
			TYPE: PRT
			ORGANISM: Homo sapiens
			US-09-800-729-215
			Query Match 11 58; Score 314; DB 10;
			Best Local Similarity 29.88; Fred. No. 9.8e-20;
			Mismatches 117; Indels 36; Gaps 10;
			Matches 88; Conservative 5;
			Query 227 LGVFGAGLSSAYIK--KLYIGRHSTDREVALMLMLMAYLSYMAELLDLSGLITYFECGIV 284
			Best Local Similarity 29.88; Fred. No. 9.8e-20;
			Mismatches 117; Indels 36; Gaps 10;
			Matches 88; Conservative 5;
			Db 1 MGAVTGCVVATVKTKLHC--FPLETALFFLMWSWSTFLLAQCGFTGVVAVLFCGQT 57
			Query 285 MSHYWHVNTYESSRTHKAPNEKITWQOQVVIWAGLARGVASYIALAYNKF 404
			Best Local Similarity 29.88; Fred. No. 9.8e-20;
			Mismatches 117; Indels 36; Gaps 10;
			Matches 88; Conservative 5;
			Db 58 QAHYTNNLVSERSRTKQLEFLHFLAENFISYMSGMLAFTFQKHVF--PIFTIG-- 112
			Query 345 SLLGLVLIGRAAFYFPLPSLFSLNLTQKAPNEKITWQOQVVIWAGLARGVASYIALAYNKF 404
			Best Local Similarity 29.88; Fred. No. 9.8e-20;
			Mismatches 117; Indels 36; Gaps 10;
			Matches 88; Conservative 5;
			Db 113 -AFVAFLGAAHYPLSFPLNLLGMDALDIEKWFASDRPKSIGTS 344
			Query 405 TRSGHTQHGNIAIMTSITVFLSTMVFGMMTKPLIRLPLPASHPTSEPPSPKSLHS 464
			Best Local Similarity 29.88; Fred. No. 9.8e-20;
			Mismatches 117; Indels 36; Gaps 10;
			Matches 88; Conservative 5;
			Db 165 ---DFASAYQRQMMFTTLLIVFETWVIIIGGTGTTMSWL---NIRGVDPDDOPPPNN 216
			Query 465 PLLTQSDFDLSLTTNIVRSPSLMLTQKPTHT--WHYWWKFDDBLMRPMFGGR 518
			Best Local Similarity 29.88; Fred. No. 9.8e-20;
			Mismatches 117; Indels 36; Gaps 10;
			Matches 88; Conservative 5;
			Db 217 DSFQLQGDG-----PSARGNRTKQESAWIFLWTSDFHNLKPLTHSG 262
			Query 18 DYASV--VSINIFVALLCAGTVLGLLLEE-NRWVNESTITAIGLCTGVVLLMFKGS 73
			Best Local Similarity 29.88; Fred. No. 9.8e-20;
			Mismatches 117; Indels 36; Gaps 10;
			Matches 88; Conservative 5;
			Db 99 DYHVRTPFETISWILLACLMKGFHVPTTISIVPESCLLIVVGLVGGGLI---KGVG 154
			Query 74 SHLFVFSSEDFLFFYLLPPLTENAGFQVKKKOFFRNFMITITLEFGAVCTMISFPTIS--IAA 131
			Best Local Similarity 29.88; Fred. No. 9.8e-20;
			Mismatches 117; Indels 36; Gaps 10;
			Matches 88; Conservative 5;
			Db 155 ETPPFLQSDVFFFLPPIIILDAFYFLLRQPTENLCTILITPAVVGTLWNAFLGGILYA 214
			Query 132 IAIFSRMNGTLDVGDFIAIGATPSATSVCTQVLVNODE-TPFLYSLVFGCVVNDAT 190
			Best Local Similarity 29.88; Fred. No. 9.8e-20;
			Mismatches 117; Indels 36; Gaps 10;
			Matches 88; Conservative 5;

RESULT 14  
 US-09-800-729-128  
 ; Sequence 128, Application US/09800729  
 ; Patent No. US20020068319A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ni et al.  
 ; TITLE OF INVENTION: 32 Human secreted proteins  
 ; FILE REFERENCE: PZ044P1  
 ; CURRENT APPLICATION NUMBER: US/09/800,729  
 ; CURRENT FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: PCT/US00/26013  
 ; PRIOR FILING DATE: 2000-09-22  
 ; PRIOR APPLICATION NUMBER: 60/155,709  
 ; PRIOR FILING DATE: 1999-09-24  
 ; NUMBER OF SEQ ID NOS: 217  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 128  
 ; LENGTH: 339  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-800-729-128

Query Match 10.7%; Score 292.5; DB 10; Length 339;  
 Best Local Similarity 29.9%; Pred. No. 6.8e-18;  
 Matches 78; Conservative 48; Mismatches 104; Indels 31; Gaps 8;

Qy 259 MAYLSYMLAELLDLSGILTVFFCGIVMSIYWHNTTESSRVTKHAFATLSFIAETFLFL 318  
 Db 1 MSWSFLLEAAGFGTGVAVLFCGTTQAHAYNNLSVESSRTRKQFEVLHFLAENFIFS 60  
 Qy 319 YVGMDALDIEKWEFASDRPKSIGISSITLLGLVIGRAAFVPLSFLSNLTKKAPNEKIT 378  
 Db 61 YMGLALFTFKHVFS -- PIFTIG --- AFAVAFGRAAHYPLSFNLGR -- HKIG 110  
 Qy 379 WRQQVVIWAGLMRGAVSTALAYNKETRSIGHTQLHGNAIMTSTITVVLFLSTVFGMKT 438  
 Db 111 WNFQHMMMFSGL-RGAMAFALAIR --- DTASYARQMMETTLLIVFTWIGGTT 163  
 Qy 439 PLIRLLPASGHPTSESSSPKSLSHSPLTSMOGSDLESITNIVRPSLRLKPTHT- 497  
 Db 164 PMLSWL --- NIRGVDPDDOPPPNNDSFOVQLQGDG --- PDSARGNRTKQESAW 210  
 Qy 498 VHYWRKFDALMRPMGGRS 518  
 Db 211 IFRLYYSFDHNLYLKPTLTHSG 231

Search completed: March 26, 2003, 18:59:21  
 Job time : 38 secs

RESULT 15  
 US-09-800-729-129  
 ; Sequence 129, Application US/09800729  
 ; Patent No. US20020068319A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ni et al.  
 ; TITLE OF INVENTION: 32 Human secreted proteins  
 ; FILE REFERENCE: PZ044P1  
 ; CURRENT APPLICATION NUMBER: US/09/800,729  
 ; CURRENT FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: PCT/US00/26013  
 ; PRIOR FILING DATE: 2000-09-22  
 ; PRIOR APPLICATION NUMBER: 60/155,709  
 ; PRIOR FILING DATE: 1999-09-24  
 ; NUMBER OF SEQ ID NOS: 217  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 129  
 ; LENGTH: 339  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-800-729-129

Query Match 10.7%; Score 292.5; DB 10; Length 339;  
 Best Local Similarity 29.9%; Pred. No. 6.8e-18;  
 Matches 78; Conservative 48; Mismatches 104; Indels 31; Gaps 8;





Matches	148:	Conservative	113:	Mismatches	95:	Indels	48:	Gaps	15;
Qy	27	LFVALCACIVGHLL-----EENRWTNESTITALLIGLCTGVVILLMTKGKSSHLFVF	79						
Db	37	LFILLY----LLIGALLTTSYVQSKKTRAIHETVSYFGVYGLIRSPGLTQNMSRP	93						
Qy	80	SEDFLEFLIPPIIFNAGFYKKOFFERNFTITLFGAVYTMISFFTISAAIAIFSRMN	139						
Db	94	HSTYFFENVLPLPIIUNSGYEHLQSNSFRNQGTLTFAGTFTISAVTGLV-LVYIFSLN	152						
Qy	140	IGLTVQG--DFAIGAIFASATDSVCTQLVNLQ---DETPLFLYSVNGEVYNDATSVLF	194						
Db	153	FENLSNTFVEALSMGATLSMATTSDPVTYLAINTNSYKDVQK--LYTIVGESTLNDATAIVMF	210						
Qy	195	NALQNFEDLVHDAAVLKPEGFNFVFLSSTPLGVYFAGLISAYIKKKLYGRHSTDREVA	254						
Db	211	ETLQFOGKTLHFETLFSGIGIFITFISLIGSIGLITALLKYSYLRPPS-TESG	269						
Qy	255	LMMMLMAYLSYMLMAELLDLSGILTTFEGTIVYMSHTWHNVTESSRVYTKAHATLSFTAET	314						
Db	270	TILLMAYTSFFNSGCHMSGVSLFCGITLKHYAFNMNSYKAULSTKYFVLQSEN	329						
Qy	315	FLEXYGMDDALDIEKWEFAASDRPGKSIGISSGFLVGLGRAAF--VFPFLSFLSNUTKKA	372						
Db	330	FIFTYLGMSLFT-----QVDLVYKPI--FILITIVAVATASYRMNVEPLSNLLNKFHRO	380						
Qy	373	PN---EKTMTRQQVVIWAWGLMRGAVSIALAYNKTRPSGHOLHNAIMTSTTIVVLF	428						
Db	381	RGNNLIDHPISYQOMLFWAGL-RGAVGVALAAGFEGNAQT-----LRATTLVWWVL	432						
Qy	429	STMVFGMMTKPLIRLPLLPAAGHPVTPSEPSPSKLHSPLLTSMQGSDLESTTNIVRSSLR	488						
Db	433	TLIIFGTTARMLEILHETG--VAADVDVSDTEIGMLPWWQOSPEFDLENSAMELSDAAE	490						
Qy	489	MLLTQPTHTVHVVWRFDDALMRYP	512						
Db	491	PVVVDQQTTER---FDEGNITAP	510						
<b>RESULT 5</b>									
Qy	569734	hypothetical protein YDR456w - yeast (Saccharomyces cerevisiae)							
C;Species:	Saccharomyces cerevisiae								
C;Date:	22-Aug-1996	#Sequence_revision	06-Sep-1996	#text_change	19-Apr-2002				
C;Accession:	S69734								
R;Dietrich, F.S.									
submitted to the EMBL Data Library, August, 1995									
A;Description: The sequence of <i>S. cerevisiae</i> lambda 3641 and cosmids 9461, 9831, and 941									
A;Reference number: S69555									
A;Accession: S69734									
A;Molecule type: DNA									
A;Residues: 1-633 <DB>									
A;Cross-references: EMBL:U33007; NID:9927685; PID:9927695; GSPDB:GN00004; MIPS:YDR456w									
C;Genetics:									
C;Superfamily: hypothetical protein yvgp									
Query Match	19.6%	Score	533:	DB	2;	Length	633:		
Best Local Similarity	26.2%	Pred.	No.	1	3e-31;				
Matches	153;	Conservative	127:	Mismatches	190:	Indels	114;	Gaps	20;
Qy	16	TSDYASVSVSINLFVALLCACIVIGHLLEEN - RWVNNESTITALIIGLCTGVVILLMTKGKS	73						
Db	55	TEEMFESSWALFMLLISALWSSYYTQKRTRAVHETVLSFYGMVGLIRMSPGHY	114						
Qy	74	SHLFFVSEDFLFFYIYLPLPIIFNAGFQVKKKOPFRNFMTITLFGAVGTMISFTTISAAIA	133						
Db	115	QDTVTFNSSYFFVNLLPLPTNSGYELQVNFFNNMNLISLIAPIGPFSAVVGI-TLY	173						
Qy	134	IFERMNIGTLDV -GDFIAIAGTATSDVCPLOVNDET -PFLYSLVGFEGVNDAT	190						





C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
 C;Accession: S30198; S29341  
 R;Counillon, L.; Pouysseur, J.  
 B;Title: Nucleotide sequence of the Chinese hamster Na(+) / H(+) exchanger NHE1.  
 A;Reference number: S30198; MUID:93192322; PMID:8383540  
 A;Accession: S30198  
 A;Molecule type: mRNA  
 A;Residues: 1-682  
 A;<CDS>  
 A;Cross-references: EMBL:X68970; PIDN:CAA48771\_1; PID:q49473  
 C;Genetics:  
 A;Gene: NHE1  
 C;Keywords: glycoprotein; ion transport; membrane protein  
 F;76\_374\_414/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 17.6% Score 478; DB 2; Length 822;  
 Best Local Similarity 28.7%; Pred. No. 2e-27;  
 Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;  
 Query Match 18 DYASV--VSINLFVALCACIVLGHLEE-NRQYNESTALIIGLCTGVVILLMTKGS 73  
 Best Local Similarity 29.2%; Pred. No. 2.7e-27;  
 Matches 149; Conservative 99; Mismatches 193; Indels 70; Gaps 20;  
 Qy 99 DYLIVRTPPEFISLWLLACIMKIGFHVIITSSIVPESCLIVVGLYGLI --- KGVG 154  
 Db 155 ETPPFLQSPVFPFLPPLDAGYFLPLRQFTENLGTIFAVGTLMNAFFGGLLYA 214  
 Qy 132 IAFSRMNIGTLDVDFLAGIANSATSVCTLVQLNQDE-TPFLYSLVGEVGVVNDATS 190  
 Db 211 VCLVGEQINNIGLDDNLFGSISIADVPAVAYFEIHINELLHLVFGESLNDAVT 270  
 Qy 191 IVLFNALQ --NFDLVHIDAAVVLKFLGNFNFYLFLSSTFLGVAGLSSAYIKKLYIGRH 247  
 Db 271 VVXLHLEEEFANYDRVGI\_DVIVGFL\_SFFVVSLLGGFVGVVGVIAFTSR --FTSH 325  
 Qy 248 STDREVALMLMLSYMLMAELLDLSGLTUVFGLVMSHTWHNTTESSRVTTKHAFAT 307  
 Db 326 IRVTEPLFVFLYSTMAYLSAEFLHSGNIALIASQVMRVEANISHSSHTTKYFLRM 385  
 Qy 308 LSFTAETFLFLYGMDALIE -- KWEFASDRPGKSIGISSILGLVIGRAAFVPLSF 364  
 Db 330 IRVTEPLFVFLYSTMAYLSAEFLHSGNIALIASQVMRVEANISHSSHTTKYFLRM 389  
 Qy 309 WSSVSETLFLFVFLYSTMAYLSAEFLHSGNIALIASQVMRVEANISHSSHTTKYFLRM 389  
 Db 367 NLTKAPNEKITTWRQQVVIWAGLMRGAVSTALAYNKTRSGTQTHLHNAMITSTTV 426  
 Db 441 N---KERIVLKPKDQFIAYGGRL-RGAQKPMCD -LMDKHKPFDLTLGKED 536  
 Qy 427 LFSTMVFGMMTKPLIRLPLPASGPVTSEPPSPKSLHSPLTSMQGSDLESTTNIVRSS 486  
 Db 493 FTTVFGQMTIRPLVDL --- AVKKKQETRSINEBHTQFLDHLLTGIED --- 542  
 Qy 487 LRMLLTQPTHTWYWWRFDDALMR 511  
 Db 543 ----- GHYHHHWK ---DKLNR 556  
 RESULT 13  
 157487  
 Na+ /H+ -exchanging protein, amiloride-sensitive - human  
 N;Alternative names: Na+/H+ antiporter; NHE-1  
 C;Species: Homo sapiens (man)  
 C;Accession: A44858; A3131  
 R;Reilly, R.F.; Hildebrandt, F.; Biemesderfer, D.; Sardet, C.; Pouyssegur, J.; Aronson, Am. J. Physiol. 261, F1088-F1094, 1991  
 A;Title: cDNA cloning and immunolocalization of a Na(+) -H+ exchanger in LLC-PK1 renal epithelial cells  
 A;Accession: A44858  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-818 <FL>  
 A;Cross-references: GB:S71135; PIDN:9240706; PIDN:AAE20633\_1; PID:9240707  
 A;Experimental source: LLC-PK1 kidney cell line  
 A;Note: sequence extracted from NCBI backbone (NCBIn:71135 , NCBIP:71136)

R;Reilly, R.F.  
 Am. J. Physiol. 261, 1088-1094, 1991  
 A;Title: cDNA cloning and immunolocalization of a Na+ /H+ exchanger in LLC-PK1 renal epithelial cells  
 A;Reference number: 146613  
 A;Accession: 146613  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-682 ; H<sup>+</sup> ; 684-818 <RE2>  
 A;Cross-references: GB:M9631; NID:9164595; PIDN:AAA31092\_1; PID:9164596  
 Query Match 17.5% Score 476; DB 2; Length 818;  
 Best Local Similarity 29.2%; Pred. No. 2.7e-27;  
 Matches 149; Conservative 99; Mismatches 193; Indels 70; Gaps 20;  
 Qy 18 DYASV--VSINLFVALCACIVLGHLEE-NRQYNESTALIIGLCTGVVILLMTKGS 73  
 Db 95 DYTHRTPPEFISLWLLACIMKIGFHVIITSSIVPESCLIVVGLGLIKAVGE -- 151  
 Qy 74 SHLFYVFSLEDFFYIPLLPIFNAGFOVKKKOFFRNFMITLFGANGTMISFFTIS--IAA 131  
 Db 152 TPPFLQSE-VFELFLPPLDAGYFLPLRQFTENLGTILFAVGTLMNAFFGGLMYA 210  
 Qy 132 IAIFSRMNIGTLDVDFLAGIANSATSVCTLVQLNQDE-TPFLYSLVGEVGVVNDATS 190  
 Db 211 VCLVGEQINNIGLDDNLFGSISIADVPAVAYFEIHINELLHLVFGESLNDAVT 270  
 Qy 191 IVLFNALQ --NFDLVHIDAAVVLKFLGNFNFYLFLSSTFLGVAGLSSAYIKKLYIGRH 247  
 Db 271 VVXLHLEEEFANYDRVGI\_DVIVGFL\_SFFVVSLLGGFVGVVGVIAFTSR --FTSH 325  
 Qy 248 STDREVALMLMLSYMLMAELLDLSGLTUVFGLVMSHTWHNTTESSRVTTKHAFAT 307  
 Db 326 IRVTEPLFVFLYSTMAYLSAEFLHSGNIALIASQVMRVEANISHSSHTTKYFLRM 385  
 Qy 308 LSFTAETFLFLYGMDALIE -- KWEFASDRPGKSIGISSILGLVIGRAAFVPLSF 364  
 Db 330 IRVTEPLFVFLYSTMAYLSAEFLHSGNIALIASQVMRVEANISHSSHTTKYFLRM 389  
 Qy 365 LSNLTKKANEKITTWRQQVVIWAGLMRGAVSTALAY --- NKPRTRSGTQTHLHNAMIT 420  
 Db 435 FIN--KFRIVLKPKDQFTIAVGGT\_RGAIAFSGHLLDKNHPMPCD -----LFLT 482  
 Qy 421 STIVVLFSTIMVFGMMTKPLIRLPLPASGPVTSEPPSPKSLHSPLTSMQGSDLESTTN 480  
 Db 493 ALITVVFIVFVQGCTIRPLVDL --- AVKKKQETRSINEBHTQFLDHLLTGIED 536  
 Qy 481 IVRSSLRMLLTKEPTHTWYWWRFDDALMR 511  
 Db 537 IC ----- GHYHHHWK ---DKLNR 552  
 RESULT 13  
 157487  
 Na+ /H+ -exchanging protein, amiloride-sensitive - human  
 N;Alternative names: Na+/H+ antiporter; NHE-1  
 C;Species: Homo sapiens (man)  
 C;Accession: 157487; A3131  
 R;Friegel, L.; Dyck, J.R.; Wang, H.; Fong, C.; Haworth, R.S.  
 Mol. Cell. Biochem. 125, 137-143, 1993  
 A;Title: Cloning and analysis of the human myocardial Na+/H+ exchanger.  
 A;Reference number: 157487; MUID:94111706; PMID:8283968  
 A;Accession: 157487  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-815 <FL>  
 A;Cross-references: GB:S68616; NID:9544775; PIDN:AAC60605\_1; PID:9544776  
 R;Sardes, C.; Franchi, A.; Pouyssegur, J.  
 Cell 56, 271-280, 1989  
 A;Title: Molecular cloning, primary structure, and expression of the human growth factor  
 A;Reference number: A31311; MUID:89106219; PMID:2536298  
 A;Accession: A31311  
 A;Molecule type: mRNA

A; Residues: 1-814; 'SNARSRQRQLSPHLFHQSRGCGWGLPLPPLTRIGAPPPTAWOLGPQPPQHSSPAASREASSPPEH						
C; Genetics:						
A; Gene: GDB:SLC9A1; APNH; NHE1						
A; Cross-references: GDB:119633; OMIM:107310						
A; Map position: 1p36.1-1p35						
C; Keywords: glycoprotein; transmembrane protein F; 75,370,410/Binding site: carbohydrate (Asn) (covalent) #status predicted						
Query Match	17.4%	Score 474;	DB 2;	Length 815;		
Best Local Similarity	28.8%	Pred. No. 3.8e-27;				
Matches	146;	Conservative	96;	Mismatches	203;	Indels 62; Gaps 19;
Qy	18	DYASY--VSINLFVALLACIVGHLLBE-NRKYNESTALIGLCLGVVILLMTKKS	73			
Db	95	DYTHVRTPPFISLWLACLMKIGFHVPIPTKISSVYPSLIVVLLGGLI	--KGVG	150		
Qy	74	SHLFVFSEDLFYIPLLPIIFNAGQVKIIRRNFMTITLGAVGTMISFFETIS--	131			
Db	151	ETPPFLQSDDFFLFLPILTDAGYFLPLRQFTENLGTLIFAVGTWNNAFFLGGLMAYA	210			
Qy	132	IAIFSRMNIIGTLDVGDFLAIGAIFSATDSVCTLQVLNQDE-TPFLYSLVFGESVNDAT	190			
Db	211	VCLVGEQIINNIGLIDNLNLLFGSIIASAVDPAVLAVEEIHINELLHIVFGESLLNDAVT	270			
Qy	191	IVLFNALQNF-DLVHDAVAVLKLFG - -NFPYLFLSSTFLGVFAGLLSAYIKKLYIGRH	247			
Db	271	VVLYHLEEEFANYEHV- -GLVDIEFLGFLSFFVVALGVLYGVVYGVIAFTSR --FISH	325			
Qy	248	STDREVALMLMAYLSSYMLAELDSLGLTUVFGCGIIVMSHTYNTVSVRTTKHAFAT	307			
Db	326	IRVTEPLFLYVGMDALIE-- KWEFASDRPGKSIGSSSISLLGLVLRGAATVFPPLSF	364			
Qy	308	LSFIAETFLFLYVGMDALIE-- KWEFASDRPGKSIGSSSISLLGLVLRGAATVFPPLSF	385			
Db	386	WSSVSETLIFLGYSTVAGSHHNNWTFV -----ISTLL --FCLLARVLGVLGLTW	434			
Qy	365	LSNLKKAPNEKTIWKRQQVVIWAGLMLRGAVSIALAYNKFRTRSGHTQLQIGNAIMITSTT	424			
Db	435	FIN--KFERIVKLTKPKDQFIAYGGL- -RGAISGUY - -LLDKKHFPMCD - -LFLTAIT	486			
Qy	425	VVLFSTIVMFGMMTKPALKRLLPASGPVTPSEPPSSPKLHSRPLKTTSMQGSDELESTNTVYRP	484			
Db	487	VIFFTVVQGMТИRLVLL-----AVKKQQTTRRSINEEHTQFLHLLTGIEDIC--	538			
Qy	485	SSLRMLLTKPTHTVHYWRFKDDALMR	511			
Db	539	-----GHYGHHHWK --DKLNR	552			
RESULT 14						
A46188	CAMP-activated Na+/H <sup>+</sup> -exchanging protein betanHE	- rainbow trout				
C; Species: Oncorhynchus mykiss (rainbow trout)						
C; Accession: A46188	C; Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997					
R; Borgetto, F.; Sardet, C.; Cappadoto, M.; Pouyssegur, J.; Matais, R.						
Proc. Natl. Acad. Sci. U.S.A. 89, 6765-6769, 1992						
A; title: Cloning and expression of a cAMP-activated Na <sup>+</sup> /H <sup>+</sup> exchanger: evidence that the						
A; Reference number: A46188; PMID:1379718						
A; Accessions: A46188						
A; Status: Preliminary; not compared with conceptual translation						
A; Molecule type: nucleic acid						
A; Residues: 1-759 <B0R>						
A; Experimental source: cephalic kidney hematopoietic tissues						
A; Note: sequence extracted from NCBI backbone (NCBIP:113525)						
RESULT 15						
Query Match	17.3%	Score 472;	DB 2;	Length 759;		
Best Local Similarity	28.7%	Pred. No. 4.9e-27;				
Matches	140;	Conservative	96;	Mismatches	188;	Indels 64; Gaps 18;
Qy	31	LICACIVL-HLLE-NRKYNESTALIGLCLGVVILLMTKGKSSHLYFVSEDLFFIYL	88			
Db	78	LLALLNKLGFLLIPRIPLAAYVPECLLIVVGLGGGLIYKIGEAPP ---VLDLSQULFFCL	133			

Qy	89	LPPITFAGFOVKKQKOFFERNFMFTIS--IAIAIAIFSRMNNITGLDVG	146
Db	134	LPPILDAGYFLPIRPFENVTILVFAVGTILWHAFFMGGLYLPCQESVGLSGVDL	193
Qy	147	DFLAIGAIFSAATSDVCTLQVNDE-TPFVLSSLVFGEGVYNDATSVLFNALQNFDLVH	205
Db	194	ACLFGSISVSAVPAAVLEBEEIHINELVHLVIGESLUNDAVTVLNFEESVKG-	252
Qy	206	DAAVLFLFLG--NFFYFLSSTFLGVFAGLISAYIKLYIGRHSTDREVALLMMAYLS	263
Db	253	TVTLDFLGIVCFVSLGGVLYGAGYLAFFTSR---FTSHTRVIEPLFLVSYNA	309
Qy	264	YMLAEFLDLDSGLTVEFCGIVMSHTWNVNTTESSRVTTKAFAATLFSIAETFLFLVYGM	323
Db	310	YLSSEMFLHLSGIMALIACGVMRPMVYEAANISHKSXTTICKFLKMWSVSETLFLFLGV	369
Qy	324	AL--DIEKWEFASDRPGKSIGTSISSLGLVLIGRAAFVFPFLSFLSNLTKKAPNKHITWR	380
Db	370	TWAGPHAWNWTTFV-----ITVYI-LCLVSRVLYGVIGLTFIN--KFRIVKLTRK	415
Qy	381	QQVYIWAGLMRGAASIALAYNKFRTRSGHTQLHGNAIMITSTIVVLFSTMFGMGTMKPL	440
Db	416	DQPTIVAGFLRGIAIASLGLY--LILSNSHONRN-LFLTAITIIFTYEVQQTIRPL	469
Qy	441	IRLLPASGHPYVTPSEPSPSKPLHSP---LLTSMQGSDLESTTNIVRPSSLRMLLTJKPHT	496
Db	470	VELL--AVKKKESKPSINEEHTEFLDHLLTGVEG-----	507
Qy	497	TVHYWRK 504	
Db	508	YGHYHWKE 515	
RESULT 15			
A4	0/0/04	Na+/H+-exchanging protein 1 - rat	
N	Alt species: Na+/H+ antiporter		
C	Species: Rattus norvegicus (Norway rat)		
D	Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 28-Feb-1997		
C	Accession: A40204		
R	Orlowski, J.; Kandasamy, R.A.; Shull, G.E.		
J	Biol. Chem. 267, 9331-9339, 1992		
A	Title: Molecular cloning of putative members of the Na/H exchanger gene family related proteins.		
A	Reference number: A40204; PMID:92250539; PMID:1577762		
A	Accession: A40204		
A	Status: preliminary		
A	Molecule type: mRNA		
A	Residues: 1-820 <OR>		
A	Cross-references: GB:M85299		
C	Keywords: transmembrane protein		
Qy	48	QNEEITALLIIGLCTGVILLMTKQKSSHFLFVRSIDLIIFYIILPPLIFNAGFOVKKKQFFR	107
Db	133	VPECLLIVGLVGGGLI---KGVGTEPPFLQSDVFELFLPPILDAVFLPLRQFTE	188
Qy	108	NEMFTITLFGAVGMISFTIS--IAATAIFSRMNNITGLDVGDFLTAIGAIFSATDSVCTLQ	165
Db	189	NLGTLILIPAVVGTILWNAFLPGLLILYAICLVGGEQINNIGLDTLPFLGSIISAVDVAVL	248
Qy	166	VLNQDE-TPFLYSLVFGEGVWNDAATSVLFNALQNF--DLVHDAVVLKFLGNFFYLF	221
Db	249	VFEETHINELVHLVIGESLNDAVTVLNFEESVKG-YVGI-SDFLGFGL-SFEVVVS	306
Qy	222	LSSFTTFLGAGLSSAYIKLYIGRHSTDREVALLMMAYLSAELLDLSGTLVFFC	281
Db	307	LGGVFGVYVGIAFTSR---FTSHTRVIEPLFLVSYNAFLHSIGNIALIAS	363

Qy 282 GIVMSHYTWHNVTTESSRVTTKHAFAFLSFIACETFLFLYVGMDAL-DIEKWEFASDRPGKS 340  
 Db 364 GIVMMPYVEANISHSHTTICKYFLRMWSSVETLIFIFLGWSTYAGSHONW-----T 416  
 Qy 341 IGISSITLGLVIGRAAFVFFPLSLSNLTKAPNEKITWQQVNTWAGLMRGAVSTALA 400  
 Db 417 FVISTL--FOLIARYLGVLWTFIN---KFRIVKLTPADQFTIAYGGGL-RGATAFSLG 470  
 Qy 401 YNKFTPSGHTQLHGNAIMTSITITVVLFSSTMVFGMMTKPLIRLLPASHPVTSBPPSPK 460  
 Db 471 Y--LLDKKKHFFMCD--LFELTAITYVFFTVVOGMTIRPLVDLL----AVKKKQETKR 520  
 Qy 461 SLHSPPLITSMQGSDLESTTNVRPSSLRMLLTKEPTHTVHYWRKFDDALMR 511  
 Db 521 SINEEHTQFDHLLTGIEDC-----GHYGHHRWK---DKUNR 556

Search completed: March 26, 2003, 18:54:19  
 Job time : 28 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	541	19.9	669	1 NAH6_HUMAN	Q92581 homo sapien
2	533	19.6	633	1 NAH2_YEAST	Q04121 saccharomyces cerevisiae
3	492	18.1	632	1 NAH2_RABBIT	P26432 oryctolagus cuniculus
4	485	17.8	809	1 NAH5_HUMAN	P50482 oryctolagus cuniculus
5	485	17.8	896	1 NAH5_HUMAN	Q14940 homo sapien
6	482.5	17.7	834	1 NAH3_HUMAN	P48764 homo sapien
7	481	17.7	816	1 NAH1_RABBIT	P23791 oryctolagus cuniculus
8	480.5	17.7	831	1 NAH3_RAT	P26433 ratmus norvegicus
9	480	17.6	812	1 NAH2_HUMAN	Q9ubyo homo sapien
10	480	17.6	839	1 NAH3_LDIDMA	P48762 didelphis marsupialis
11	479	17.6	813	1 NAH2_RAT	P48763 ratmus norvegicus
12	479	17.6	820	1 NAH1_MOUSE	Q61165 mus musculus
13	479	17.6	898	1 NAH5_RAT	P320x2 ratmus norvegicus
14	478	17.6	822	1 NAH1_CRIGR	P48761 cricetus leucurus
15	476	17.5	817	1 NAH1_BOVIN	Q28036 bos taurus
16	476	17.5	818	1 NAH1_PIG	P26431 rattus norvegicus
17	476	17.5	820	1 NAH1_RAT	P19634 homo sapien
18	474	17.4	815	1 NAH1_HUMAN	Q01345 oncorynchus leucurus
19	472	17.3	759	1 NAH2_LONCHY	P26434 rattus norvegicus
20	456	16.8	717	1 NAH4_RAT	O16452 canenorhabdus elegans
21	395	14.5	651	1 NAH3_CAEEL	P35449 canenorhabdus elegans
22	390	14.3	667	1 NAH9_CAEEL	Q50678 mycobacterium tuberculosis
23	236.5	8.7	542	1 YM87_MYCTU	P32703 escherichia coli
24	231	8.5	549	1 YMCE_ECOLI	P76007 escherichia coli
25	186.5	6.9	578	1 YGCO_ECOLI	Q42701 zygosaccharomyces pombe
26	159	5.8	808	1 NAH2_ZYGRO	Q60362 methanococcus marcusii
27	142.5	5.2	426	1 Y057_METJUA	Q99173 zygosaccharomyces kudriavzevii
28	140.5	5.2	791	1 NAH1_2ZYGRO	Q9y289 homo sapien
29	139.5	5.1	635	1 SL56_HUMAN	P26335 enterococcus faecalis
30	138.5	5.1	383	1 NAPA_ENTHR	Q99271 saccharomyces cerevisiae
31	137.5	5.1	985	1 NAH1_YEAST	Q58916 methanococcus marcusii
32	133.5	4.9	422	1 YF21_METJUA	P31077 wolinella sphaeroides
33	131.5	4.8	759	1 PSRC_WOLSUS	

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SwissProt\_40 : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

## Result No.:

SEQUENCE OF 4-669 FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE=9175963; PubMed=9507001;

Numata M., Petrecca K., Lake N., Orlowski J.;

"Identification of a mitochondrial Na+/H+ exchanger.";

J. Biol. Chem. 273: 6951-6959 (1998).

[2]

SEQUENCE OF 4-669 FROM N.A.

SEQUENCE=9179154; PubMed=903902;

RX MEDLINE=9175963; PubMed=9507001;

RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,

RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;

RT "Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain.";

RL DNA Res. 3:321-329 (1996).

CC FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS FOR NA+ AND K+ ACROSS THE MITOCHONDRIAL INNER MEMBRANE. CONTRIBUTES TO ORGANELLAR VOLUME.

CC SUBCELLULAR HOMOSTASIS.

CC SUBCELLULAR LOCALIZATION: Integral membrane protein. Mitochondrial.

CC TISSUE SPECIFICITY: Ubiquitous; but is most abundant in

CC MITOCHONDRION-RICH TISSUES SUCH AS BRAIN, SKELETAL MUSCLE, AND

CC HEART.

CC SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

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CC -----

CC EMBL: D87743; BAA13449.1; -.

DR Genew; HGNC; 11079; SLC9A6.

DR InterPro; IPR000676; NAH\_Exchngr.

DR InterPro; IPR004709; NAH\_exchng3.

DR PRIMs; PFO0939; Na+\_H+\_Exchanger ; 1.

DR PRIMs; PR01084; NAHECHNGR.

DR TIGRFAMS; TIGR00840; b\_cpal; 1.

DR Transmembrane; Transport; Antiport; Sodium transport; Sodium

KW Mitochondrion.

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: March 26, 2003, 18:42:04 ; Search time 27 seconds  
(without alignments)  
821.816 Million cell updates/sec

Title: US-09-888-035A-2

Perfect score: 2722

Sequence: 1 MGMEVAARL GALTTSDYA.....GRGFVFPSPGSPTEQSHGGR 535

## ALIGNMENTS

## RESULT 1

NAH6\_HUMAN

ID NAH6\_HUMAN

STANDARD

PRT:

669 AA.

AC

09281;

CREATED

30-MAY-2000 (Rel. 39, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

DE

Sodium/hydrogen exchanger 6 (Na(+)/H(+)) exchanger 6 (NHE-6).

GN

SLC9A6 OR NHE6 OR KIAA0267.

OS

Homo sapiens (Human).

RA

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Primates;

OC

NCBI\_TaxID=9606;

RN

SEQUENCE FROM N.A.

RX MEDLINE=9179154; PubMed=903902;

RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,

RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;

RT "Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain.";

RT DNA Res. 3:321-329 (1996).

CC FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS FOR NA+ AND K+ ACROSS THE MITOCHONDRIAL INNER MEMBRANE. CONTRIBUTES TO ORGANELLAR VOLUME.

CC THE MITOCHONDRIAL HOMOSTASIS.

CC SUBCELLULAR LOCALIZATION: Integral membrane protein. Mitochondrial.

CC TISSUE SPECIFICITY: Ubiquitous; but is most abundant in

CC MITOCHONDRION-RICH TISSUES SUCH AS BRAIN, SKELETAL MUSCLE, AND

CC HEART.

CC SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

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CC -----

CC EMBL: D87743; BAA13449.1; -.

DR Genew; HGNC; 11079; SLC9A6.

DR InterPro; IPR000676; NAH\_Exchngr.

DR InterPro; IPR004709; NAH\_exchng3.

DR PRIMs; PFO0939; Na+\_H+\_Exchanger ; 1.

DR PRIMs; PR01084; NAHECHNGR.

DR TIGRFAMS; TIGR00840; b\_cpal; 1.

DR Transmembrane; Transport; Antiport; Sodium transport; Sodium

KW Mitochondrion.

FT	TRANSMEM	28	48	POTENTIAL.	OX
FT	TRANSMEM	71	91	POTENTIAL.	RN [1]
FT	TRANSMEM	103	123	POTENTIAL.	RP SEQUENCE FROM N.A.
FT	TRANSMEM	142	162	POTENTIAL.	RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A., Carpenter J.J., Chen E., Cherry J.M., Chung E., Duncan M., Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M., Shroff N., Winant A., Yelton M., Botstein D., Davis R.W.; Submitted (AUG-1995) to the EMBL/GenBank/DDJB databases.
FT	TRANSMEM	179	199	POTENTIAL.	RN [2]
FT	TRANSMEM	220	240	POTENTIAL.	RP
FT	TRANSMEM	246	266	POTENTIAL.	RA
FT	TRANSMEM	292	312	POTENTIAL.	RA
FT	TRANSMEM	340	360	POTENTIAL.	RA
FT	TRANSMEM	382	402	POTENTIAL.	RA
FT	TRANSMEM	404	424	POTENTIAL.	RL
FT	TRANSMEM	447	467	POTENTIAL.	RL
FT	TRANSMEM	483	503	POTENTIAL.	RN
SQ	SEQUENCE	669	AA:	74161 MW: F6416596229F2639 CRC64;	RP
				MEDLINE=98175563; PubMed=9507001;	RX
				"Identifies a mitochondrial Na+/H+ exchanger.";	RT
				J. Biol. Chem. 273:6951-6959(1998).	RL
QY	1	MGMGEVAAAARLGALYTSDYASVVSINLEVALICACTYLGHILLEEN - RWNESITALLIG	58	- FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS FOR NA+ AND K+ ACROSS THE MITOCHONDRIAL INNER MEMBRANE. CONTRIBUTES TO ORGANELLAR VOLUME AND CALCIUM HOMEOSTASIS.	CC
Db	53	MDEBEIVSEKQAEEPSHRSANIL--I	1	- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.	CC
QY	59	LCTGVV-----ILLMTKGKSSH--LLEVSEDFFIYLAPPILFNAGFOVKK	102	- SIMILARITY: BELONGS TO THE Na(+)/H(+) EXCHANGER FAMILY.	CC
Db	110	LLVGLVLRYGHIVPSDVNNVTISCEVOSSPPTLLVTFDPEEFNILLPPIFYAGYSLKR	169	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> )	CC
QY	103	KQFERNFMNTITLFGAVGTMISFFTISIAIAFSRNRNLTGDFE----LAIGAFSA	157	CC	
Db	170	RHFERNLGSILAYAFLGTAISCFVGISSYCVTLNKVTGGLAGDFYFTDCLLFGAIVSA	229	CC	
QY	158	TDSVCTLQVINQDETTPF-LYSVLFGEVVNDATSVIFNALQNF---DLVH-IDAAVVL	211	CC	
Db	230	TDPVTVLIAIEBLQDVELYAILFQGIVLNAAVATVLSSSVYQAGDFTYDAM	289	DR ENBL: U33007; AA64861-1; -.	DR
QY	212	KFLGNFVFYLFSLSSTFLGVFAQLLSAYTIK-KLYIGRHSRTHREVALMMNAYLSYMAEL	269	DR InterPro: IPR00676; NAH_Exchngr.	DR
Db	290	KSIGIPLGIGFSFAMGAATECVTALVTKETKL--REFQLEIGFLFEMWSITFLAEA	346	DR InterPro: IPR00709; Na_H_Exchngar; 1.	DR
QY	270	LDLGLSLTVFCFCGIVMSHYTHWHNVTESSRVTKHAFATLSFTAETFLFLYVGMDALDIK	329	DR PRINTS: PRO1084; NAHECHNGR.	DR
Db	347	WGFTGVAVLQFLPGCGITQAHYTTNLLTESQHRTKQFELLNFNAENFISYMLGTLPFTFQN	406	KW TIGRFAMS; TIGR00840; b_cpa1; 1.	KW
QY	330	WEFASDRPGKSGKSIQSSILLGVLGRAAFYPLSPLSNLTKAPNEKTIWROQVYIWAG	389	KW Transmembrane; Transport; Antiport; Sodium transport; Mitochondrion.	KW
Db	407	HVF---NPFTVVG---AFVAFILGRAAINTYPLSLLNIGRS---KIGSNFQIMMMFAG	456	FT TRANSMEM 62	FT
QY	390	LMRGAVSIALAYNKETRSQHTQLHGNAINMTTITIVLFLSTMVFGMMTQPLIRLPLLQAG	449	FT TRANSMEM 86	FT
Db	457	L-RGAMAFALAIR----DTATIAROMMFSTTLLIVFFTVWFGGTITAMLSCL-----	504	FT TRANSMEM 118	FT
QY	450	HPVNSEPSSPKLSHSPSLTSMQGSDLESTNTVPRSSLMLTRPHTVHYWRKFDDA	509	FT TRANSMEM 154	FT
Db	505	HIVRGVDSDQEHLGVP-----ENERRTKAESAWLFRM-----WYNFDHNY	545	FT TRANSMEM 177	FT
QY	510	MRPMEGGRG 518		FT TRANSMEM 218	FT
Db	546	LKPILTHSG 554		FT TRANSMEM 238	FT
				FT TRANSMEM 259	FT
				FT TRANSMEM 307	FT
				FT TRANSMEM 327	FT
				FT TRANSMEM 353	FT
				FT TRANSMEM 377	FT
				FT TRANSMEM 432	FT
				FT TRANSMEM 452	FT
				FT TRANSMEM 458	FT
				SQ SEQUENCE 633 AA: 70147 MW: 9B771ABD541CEB0A CRC64;	SQ
				Query Match Score 533; DB 1; Length 633;	
				Best Local Similarity 26.2%; pred. No. 1..e-27;	
				Matches 153; Conservative 127; Mismatches 190; Indels 114; Gaps 20;	
QY	16	TSDYASVVSINLVALLACIVLGHLLEN--RWVNESTITALIGLCTGVVILLMTKGKS	73	QY 16 SHLEFVSEDLFFFLYLLPLPILNAGFOVKKOFFPENMFTLFGAVGTMISFFTISIAIA 133	QY
Db	55	TEEMESSWALFIMULLLISALWSSYLLQKRITAVHETVLSIFGMVIGLIIRMSPGHY 114		Db 115 QDFTVTFNSSYFFNVLPPLPILNQGYELQVNFFNMMSLIFAPGFTISAVVIGI-TLY 173	Db
QY	74	SHLEFVSEDLFFFLYLLPLPILNAGFOVKKOFFPENMFTLFGAVGTMISFFTISIAIA 133		QY 74 IVLFNALQNFNDLVHDAAVVLFGLNFVFLSSTFLGAGLSSAYTIKKLVIGRHSTD 250	QY
Db	134	IFSRMNIGTLDV-GDFELAIGAISATSVCTLQVQNQDET-PFLYSLVFGEGVWNNTS 190		Db 174 IWTFLGLSESIDFADAMSGATLSATPVTLSIFNAYKVDPKLTYTIFGESLLNDA 233	Db
QY	30	DT 30-MAY-2000 (Rel. 39, Created)		QY 191 IVLFNALQNFNDLVHDAAVVLFGLNFVFLSSTFLGAGLSSAYTIKKLVIGRHSTD 250	QY
Db	30	DT 30-MAY-2000 (Rel. 39, Last sequence update)		Db 234 IVMFETCQFHGPATSVSVERGAGELMTFSVSLLIGVLTGILVALLKHTHIRR PY 292	Db
DE	DE	DE Mitochondrial sodium/hydrogen exchanger (Mitochondrial Na(+)/H(+) exchanger).			
DE	DE	DE NHX2 OR NHX1 OR YDR456W OR D9461_40.			
OS	OS	OS Saccharomyces cerevisiae (Baker's yeast).			
OC	OC	OC Fungi; Ascomycota; Saccharomycetaceae; Saccharomyces.			
OC	OC	OC Saccharomyces cerevisiae; Saccharomycetaceae; Saccharomyces.			
QY	251	REVALMMLMAYLSYMLAEFLDLSGILTIVFCGIVMSHYTWINVTESSRVTKHAFATLSF	310		QY

## RESULT 2

NAH2\_YEAST

ID NAH2\_YEAST

STANDARD

PRT; 633 AA.

PRT;

633 AA.

PRT;

633 AA.

PRT;

633 AA.

PRT;

633 AA.

PRT;

633 AA.

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633 AA.

PRT;

633 AA.

PRT;

633 AA.

PRT;

633 AA.

Db 293 IESCLLIILATESYFFNSGCHMSIVSLFCGITLKHAYANNMRSQITIKYFQLLAR 352 PRINTS; PRO1084; NAHEXCHNGR;  
 DR DR TIGR0084; b\_cpal; Transport; Antiport; Sodium transport;  
 KW Transmembrane; Glycoprotein; Transport; Antiporomism.  
 KW Multigene family; Phosphorylation; CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 1 11  
 FT TRANSEM 12 27 MI (POTENTIAL).  
 FT DOMAIN 28 59 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 60 79 M2 (POTENTIAL).  
 FT DOMAIN 80 81 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 82 101 M3 (POTENTIAL).  
 FT DOMAIN 102 110 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 111 130 M4 (POTENTIAL).  
 FT DOMAIN 131 134 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 135 154 M5 (POTENTIAL).  
 FT DOMAIN 155 180 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 181 200 M6 (POTENTIAL).  
 FT DOMAIN 201 209 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 210 229 M7 (POTENTIAL).  
 FT DOMAIN 230 250 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 250 269 M8 (POTENTIAL).  
 FT DOMAIN 270 298 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 299 319 M9 (POTENTIAL).  
 FT DOMAIN 320 339 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 340 359 M10 (POTENTIAL).  
 FT DOMAIN 360 366 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 367 385 M11 (POTENTIAL).  
 FT DOMAIN 386 425 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 436 455 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 456 832 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 144 L -> P. 1  
 SQ SEQUENCE 832 AA; 8C8BB7296CFB740 CRC64;

RESULT 3  
 ID NAH3\_RABIT STANDARD; PRY; 832 AA.  
 AC P24342;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sodium/Hydrogen exchanger 3 (Na(+)/H(+) exchanger 3) (NHE-3).  
 GN SLC2A3 OR NHE3.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 RN [1]\_TAXID=9386;  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=New Zealand white; TISSUE-Ileal villus, and kidney cortex;  
 RX MEDLINE=13744392;  
 RA Tse C.-M., Brant S.R., Walker S.S., Pouyssegur J., Donowitz M.;  
 RT "Cloning and sequencing of a rabbit cDNA encoding an intestinal and  
 kidney-specific Na(+)/H(+) exchanger isoform (NHE-3)." ;  
 RL J. Biol. Chem. 267:9340-9346 (1992).  
 CC - FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED  
 CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL  
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD  
 CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL  
 CC TRANSDUCTION.  
 CC - SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.  
 CC - CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC  
 CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.  
 CC -

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 or send an email to license@lsb-sib.ch).

EMBL; M87007; AAA31420.1; -  
 DR DR A40205; A40205.  
 DR InterPro; IPR000676; NAH\_Exchngr.  
 DR InterPro; IPR004709; NAH\_Exchang3.  
 DR Pfam; PF00999; Na\_H\_Exchanger; 1.

RESULT 4  
 NAH2\_RABIT  
 ID NAH2\_RABIT

STANDARD; PRT; 809 AA.

AC P50482;	FT TRANSMEM	459	479	M (M1) (POTENTIAL).
DT 01-OCT-1996 (Rel. 34, Created)	FT DOMAIN	480	809	CYTOPLASMIC (POTENTIAL).
DT 01-OCT-1996 (Rel. 34, Last sequence update)	FT CARBOHYD	350	350	N-LINKED (GLCNAC (POTENTIAL)).
DT 15-JUN-2002 (Rel. 41, Last annotation update)	SQ SEQUENCE	809 AA:	90744 MW:	DBD00B4543D87A6 CRC64;
DE Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger 2) (NHE-2).				
GN SLC9A2 OR NHE2.				
OS Oryctolagus cuniculus (Rabbit).				
EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.				
OC NCBI_TaxID=9986;				
OX OX [1];				
RN RP SEQUENCE FROM N.A.				
RC STRAIN-New Zealand white.				
RA MEDLINE-93280159; PubMed-7685025;				
RA Tse C.-M., Levine S.A., Yun C.H., Montrose M.H., Little P.J., Donowitz J., Donowitz M.,				
RA "Cloning and expression of a rabbit cDNA encoding a serum-activated ethylisopropylamiloride-resistant epithelial Na+/H+ exchanger isoform (NHE-2)."				
RT J. Biol. Chem. 268:11917-11924 (1993).				
CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN COLONIC SODIUM ABSORPTION.				
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.				
CC -!- TISSUE SPECIFICITY: HIGH LEVELS IN INTESTINE AND KIDNEY.				
CC -!- PTM: PHOSPHORYLATED (POSSIBLE).				
CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.				
CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.				
CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				
CC -!- EMBL; L13733; ; NOT_ANNOTATED_CDS.				
DR InterPro; IPR000676; NaH_Exchnt.				
DR InterPro; IPR000709; NaH_exchang3.				
DR Pfam; PF00999; Na_H_Exchanger_1.				
DR TIGRFAMS; TIGR00840; NaHXCHNRR.				
KW Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport; Multideme family; Phosphorylation.				
FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 17 37 A (M1) (POTENTIAL).				
FT DOMAIN 38 79 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 80 100 B (M2) (POTENTIAL).				
FT DOMAIN 101 106 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 107 127 C (M3) (POTENTIAL).				
FT DOMAIN 128 138 EXTRACELLULAR (POTENTIAL).				
FT TRANSMEM 139 159 D (M4) (POTENTIAL).				
FT DOMAIN 160 168 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 169 189 E (M5) (POTENTIAL).				
FT DOMAIN 190 208 EXTRACELLULAR (POTENTIAL).				
FT TRANSMEM 209 229 F (M5A) (POTENTIAL).				
FT DOMAIN 230 236 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 237 257 G (M5B) (POTENTIAL).				
FT DOMAIN 258 277 EXTRACELLULAR (POTENTIAL).				
FT TRANSMEM 278 298 H (M6) (POTENTIAL).				
FT DOMAIN 299 307 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 308 328 I (M7) (POTENTIAL).				
FT DOMAIN 329 360 EXTRACELLULAR (POTENTIAL).				
FT TRANSMEM 361 381 J (M8) (POTENTIAL).				
FT DOMAIN 382 391 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 392 412 K (M9) (POTENTIAL).				
FT DOMAIN 413 429 EXTRACELLULAR (POTENTIAL).				
FT TRANSMEM 430 450 L (M10) (POTENTIAL).				
FT DOMAIN 451 458 EXTRACELLULAR (POTENTIAL).				

RA	Menon A.G.; "Molecular cloning and physical and genetic mapping of a novel human Na <sup>+</sup> /H <sup>+</sup> exchanger (NHE5/SLC9A5) to chromosome 16q22.1." Genomics 25:615-622(1995).	QY	246 RHSTDREVALMMILMAYLSYMIAELLDLSGLTIVFFCGITVMSHYTWHNVTESSRVTKHAF 305
RT	"-1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION (BY SIMILARITY).	Db	278 ----IEPLLIVEAYAYAAYLTTMASLISAIATVTCGKRYVEANISHSRTTKYTM 332
RL	"-1- SUBCELLULAR LOCATION: Integral membrane protein.	QY	306 ATLSFIAETFLFLYGMDALIEKWEFASDRPGKSIGISSILIG--LVLIGRAAVFVPL 362
CC	"-1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, TESTIS, SPLEEN, AND SKELETAL MUSCLE.	Db	333 KTLASCAETVIMLGTSAVDSSKKWAND-----SGLVLTGTLIFRLGVYLQ 382
CC	"-1- PTM: PHOSPHORYLATED (POSSIBLE).	QY	363 SFLSNLTKKAPNEFKITWROQYIWIAGRMGSVIALAYNKFTRSQHTQLIGNAIMTST 422
CC	"-1- CAUTION: THE NUMBER LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)H(+) EXCHANGERS VARY AMONG AUTHORS.	Db	383 TWLNLNFRVLPDKI---DQVMWSYGG-LGAVAFALV---ILLDFTKVPAKDYFVATT 434
CC	"-1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to licensed@isb-sib.ch).	QY	423 ITVVYLESTMVFGMMTKPLIR-LLLPASGHPTSEPPSPSKLHSPLTSMOGSDELSTNTI 481
CC	"-1- DR: AF111173; AAC9896_1; EMBL: U08607; AA87678; 1. DR: Genew; HGNC:11078; SLC9A5.	Db	435 IVVVFETVIVQGTIKPKYWKVKSRSH---HKPTLNQELIHTFDH----LAAYEDV 487
CC	"-1- DR: IPR000676; NaH_Exchngr.	QY	482 VRPSSLRMLLTKPTVHY---WRKFD----DALMR 511
CC	"-1- DR: InterPro; IPR004709; NH_exchang3.	Db	488 V-----GHHGYHYWRDRWEQDKYKSQLLMR 514
CC	"-1- DR: PR01084; NAEHXCHNR.	RESULT 6	
CC	"-1- DR: TIGRFAMS; TIGR00840; b_cpal; 1. KW Multigene family; Glycoprotein; transport; Antiport; Sodium transport; FT TRANSMEM 46 POTENTIAL. Phosphorylation.	ID	NAH3_HUMAN STANDARD; PRT: 834 AA.
KW	"-1- FT TRANSMEM 46 POTENTIAL. Phosphorylation.	AC	P48764.
FT	"-1- FT TRANSMEM 74 66 POTENTIAL. Phosphorylation.	RP	SEQUENCE FROM N.A.
FT	"-1- FT TRANSMEM 104 124 POTENTIAL. Phosphorylation.	RC	SEQUENCE FROM N.A.
FT	"-1- FT TRANSMEM 135 155 POTENTIAL. Phosphorylation.	RX	TISSUE=Kidney cortex;
FT	"-1- FT TRANSMEM 174 194 POTENTIAL. Phosphorylation.	RA	Medline=95358265; PubMed=7631746;
FT	"-1- FT TRANSMEM 201 221 POTENTIAL. Phosphorylation.	RT	Brant S.R., Yun C.H., Donowitz M., Tse C.-M.;
FT	"-1- FT TRANSMEM 247 267 POTENTIAL. Phosphorylation.	RT	"Cloning, tissue distribution, and functional analysis of the human Na <sup>+</sup> /H <sup>+</sup> exchanger isoform, NHE3."
FT	"-1- FT TRANSMEM 277 297 POTENTIAL. Phosphorylation.	RL	Am. J. Physiol. 269:C198-C206(1995).
FT	"-1- FT TRANSMEM 332 352 POTENTIAL. Phosphorylation.	CC	-!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ENVIRONMENTAL BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION
FT	"-1- FT TRANSMEM 361 381 POTENTIAL. Phosphorylation.	CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.
FT	"-1- FT TRANSMEM 399 419 POTENTIAL. Phosphorylation.	CC	-!- PTM: PHOSPHORYLATION (POSSIBLE).
FT	"-1- FT TRANSMEM 429 449 POTENTIAL. Phosphorylation.	CC	-!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
FT	"-1- FT CABBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
FT	"-1- FT CABBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-
FT	"-1- FT CONFLICT 202 202 L->V (IN REF. 2).	CC	-
FT	"-1- FT SEQUENCE 896 AA: 99011 MW: B9234BF0922269 CRC64;	CC	-
Query	Query Match 17.8%; Best Local Similarity 29.9%; Matches 155; Conservative 93; Mismatches 190; Indels 80; Gaps 22;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch)
Db	22 VV1NLFAFLACTVHLLE--NRYNNESTALIINGLCLGVLIMTCKSSHIFVFS 80	DR	EMBL: U28043; AAB48940_1; Genew; HGNC:11073; SLC9A3.
Db	49 LVAWLWLASLAK--IVHLSRKVTSVLPESCLLILGVLGGIVIAVAKKAEYQL--E 103	DR	InterPro: IPR000676; NaH_Exchngr.
QY	81 EDLFFIYLPPTFINAGGFOVKKKOFFRNFMFTLFGAVGTMISFFSTA-----AAI 134	DR	InterPro: IPR004709; NaH_Exchngr.
Db	104 PGTEFLFLPPIVLDGEMPSLFFDNLGAITYAVGTLWNLQAGLV 163	DR	Prints: PRO099; NaH_Exchngr.
QY	135 FSRMNIGTLDVGDELAIGAIISATDSVTCLOVLNQ--DETFPLSYLVFGVVNDATSI 191	DR	Prints: PRO084; NaH_Exchngr.
Db	164 APRVQAGL--DFLFLFSLISAVDPAVLA/FEVHVNET--LFLLVGESSLNDAVTV 218	DR	TIGRFAMS: TIGR00840 b_cpal; 1 Transmembrane; Glycoprotein; Multidomain family; phosphorylation.
Qy	192 VLFNALQNF--DLVHDAVWLFKLGFNGVLSSTLFLGTYEAGL--TSAVTTKRYIG 245	KW	DOMAIN 1 12 DOMAIN 1 12 DOMAIN 1 12
Db	219 VLYKVCNSFVEMGSANVQATDYLKGVASLFLVSLGGAVAGLVFAFLLA/TRETCKVRV- 277	FT	CYTOSMATIC (POTENTIAL). A (M1) HYDROPHOBIC.

FT	DOMAIN	25	54	Sodium/hydrogen exchanger 1 (Na(+)/H(+)) exchanger 1 (NHE-1).
FT	DOMAIN	55	73	SLC9A1 OR NH1.
FT	DOMAIN	74	79	Oryctolagus cuniculus (Rabbit).
FT	TRANSMEM	80	99	OS
FT	DOMAIN	100	112	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
FT	TRANSMEM	113	133	OC
FT	DOMAIN	134	139	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
FT	TRANSMEM	140	160	OC
FT	DOMAIN	161	180	NCBI_TaxID=986;
FT	TRANSMEM	181	202	OX
FT	DOMAIN	203	210	[1]
FT	TRANSMEM	212	232	SEQUENCE FROM N.A.
FT	DOMAIN	233	252	STRAIN-New Zealand white; TISSUE=ileal villus;
FT	TRANSMEM	253	274	REMEDINE=91293066; PubMed=1712287;
FT	DOMAIN	275	290	Tse C.-M., Ma A.-I., Yang V.-W., Watson A.-J.M., Levine S.-
FT	TRANSMEM	291	309	Montrose M.H., Potter J., Sardet C., Pouyssegur J., Donowitz M.;
FT	DOMAIN	310	340	"Molecular cloning and expression of a cDNA encoding the rabbit ileal
FT	TRANSMEM	341	362	villus cell basolateral membrane Na+/H+ exchanger.";
FT	DOMAIN	363	369	RA
FT	TRANSMEM	370	390	RA
FT	DOMAIN	391	405	RA
FT	DOMAIN	406	426	"Cloning, sequence, and tissue distribution of a rabbit renal Na+/H+
FT	TRANSMEM	427	435	RT
FT	DOMAIN	436	456	exchanger transcript";
FT	TRANSMEM	457	834	RT
FT	CARBODY	241	241	RL
FT	CARBODY	326	326	biochim. biophys. Acta 1129:105-108(1991).
SQ	SEQUENCE	834 AA:	92907 MW:	RP
			3E7E33D65DF36F7 CRC64;	SEQUENCE FROM N.A.
				RC
				TISSUE-Kidney;
				REMEDINE=92096447; PubMed=1661611;
				Hildebrandt F., Pizzonia J.H., Reilly R.F., Reboucas N.A.,
				Sardet C., Pouyssegur J., Slayman C.W., Aronson P.S., Igarashi P.;
				"Molecular cloning and expression of a cDNA encoding the rabbit ileal
				villus cell basolateral membrane Na+/H+ exchanger.";
				[2]
				RP
				SEQUENCE FROM N.A.
				RC
				SEQUENCE FROM N.A.
				RA
				SEQUENCE OF 472-816 FROM N.A.
				RA
				STRAIN-New Zealand white; TISSUE=Heart muscle;
				REMEDINE=91138752; PubMed=1748846;
				RA
				Fiegele L., Sardet C., Pouyssegur J., Barr A.;
				"Identification of the protein and cDNA of the cardiac Na+/H+ exchanger.";
				RT
				FEBS Lett. 279:25-29(1991).
				CC
				--!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION.
				CC
				--!- SUBCELLULAR LOCATION: Integral membrane protein.
				CC
				--!- TISSUE SPECIFICITY: KIDNEY AND INTESTINE.
				CC
				--!- PTM: PHOSPHORYLATED (POSSIBLE).
				CC
				--!- SIMILARITY: BELONGS TO THE (NA(+)/H(+)) EXCHANGER FAMILY.
				CC
				--!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+)) EXCHANGERS VARY AMONG AUTHORS.
				CC
				--!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
				CC
				--!- DR EMBL: X59935; CAA42558_1; -
				--!- DR EMBL: X61504; CAA43721_1; -
				--!- DR EMBL: X56536; CAA39881_1; -
				--!- DR PIR: S13926; S13926;
				--!- DR S16328; S16328;
				--!- DR InterPro: IPR00676; NaH_Exchang,
				--!- DR InterPro: IPR00709; NaH_exchang,
				--!- DR Pfam: PF00999; Na_H_Exchanger;
				--!- DR PRINTS: PRO1084; NAHEXCHNGR,
				--!- DR TIGRFams: TIGR0810; b_cpal;
				--!- KW Multigene family; Glycoprotein Transport; Antipart; Sodium transport;
				--!- FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
				--!- FT TRANSMEM 16 35 M1 (POTENTIAL)
				--!- FT DOMAIN 36 107 EXTRACELLULAR (POTENTIAL).
				--!- FT TRANSMEM 108 127 M2 (POTENTIAL).
				--!- FT DOMAIN 128 129 CYTOPLASMIC (POTENTIAL).
				--!- FT TRANSMEM 130 149 M3 (POTENTIAL).
				--!- FT DOMAIN 150 154 EXTRACELLULAR (POTENTIAL).
				--!- FT TRANSMEM 155 174 M4 (POTENTIAL).
				--!- FT DOMAIN 155 191 CYTOPLASMIC (POTENTIAL).
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FT TRANSMEM 192 211 M5 (POTENTIAL).  
 FT DOMAIN 212 227 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 228 247 M5A (POTENTIAL).  
 FT TRANSMEM 248 256 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 257 276 M5B (POTENTIAL).  
 FT TRANSMEM 276 294 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 295 315 M6 (POTENTIAL).  
 FT TRANSMEM 316 338 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 339 358 M7 (POTENTIAL).  
 FT TRANSMEM 359 386 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 387 406 M8 (POTENTIAL).  
 FT TRANSMEM 407 410 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 411 430 M9 (POTENTIAL).  
 FT TRANSMEM 431 480 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 481 500 M10 (POTENTIAL).  
 FT TRANSMEM 501 816 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 75 75 N-LINKED (GLCNAC, . . .) (POTENTIAL).  
 FT CARBOHYD 370 370 N-LINKED (GLCNAC, . . .) (POTENTIAL).  
 FT CONFLICT 242 242 V->A (IN REF. 2).  
 FT CONFLICT 569 569 K->E (IN REF. 2).  
 SQ 816 AA: 90/17 MW: 336738D267F7436 CRC64:

Query Match 17.7% Score: 481; DB: 1; Length: 816;  
 Best Local Similarity 29.2%; Pred. No. 3\_5e-24;  
 Matches 148; Conservative 96; Mismatches 201; Indels 62; Gaps 19;

QY 18 DYASV--VSINIFVALCAGTCUGHLE--NRWNESITALLIGLCTGVVILMTKGKS 73  
 DB 95 DTHVRTRPFEEISWILACLMIGFHTPTTSSIVPSCLLIVVGILVGGLI---KGVG 150  
 DB 211 VCLVGGQINNIGLDNLFLGSIISAVDPAVLAPEEIHINELLHTVEGESLLNDAVT 270  
 QY 74 SHLEVFSDDLFYIYLPLPILIFNAGFOVKKKOFFRNEMTITLGAVGTMISFTIS-IAA 131  
 DB 151 EKPPFLQEVFFEVFFELPLPTIADGYFPLRQTTENGLTLLFAVWTLNNAFFGLGMYA 210  
 QY 132 TATFSRMNTGTLGDFLAGIAFSATVSPCVLQINQDE-TPLVLSFGVGVNQD 190  
 DB 271 VVLVHLFEFANDDHVG1-VDIVLGFL SFFVALGGFVGVYGVIAFTSR---FTAH 325  
 QY 191 IVLNALQ---NFDLVHDAAVYLKLKGNNFYLFLSSLTFLGVAGLSEAYLIKLYIGRH 247  
 DB 326 IRTEPLVFLYPMAYSAELFLHSGMIALASGVYMPYHKSHTTIKFJKM 385  
 QY 308 LSFIAETFLFLYGMDALIE--KWEFASDRPGKSTGISSLLGLVLIBGRAFVFPLSF 364  
 DB 386 WSSVSETLFLIFLGVSTVAGSHHNWNTV---TISTLL-FCLLARYVLGVIGLTW 434  
 QY 365 LSNTTKAPNEKITWROQVVIWAGLMLGAVSTALAYNKFTNSGHTQIQLGNIAIMITSTIT 424  
 DB 435 FIN---KFIRVKLTPKDQFLIAIGGL-RGAIAFLSPLKSLHPSPLTSMCSDLEBTNSTNVRP 484  
 QY 425 VVLFSTMWFGMMTKPLIRLNLPLPSAGHPVTESSPSSPLKSLHPSPLTSMCSDLEBTNSTNVRP 484  
 DB 487 VIFFFWVQGMTRPLVDL---AVKKQKETKRSINEEHTQFLDHLLGIEDIC-- 538  
 QY 485 SSLRMLLTKPTHTHYWNKFKDALLMR 511  
 DB 539 ----- -GHYGHHHWK---DKLNR 552

RESULT 8  
 NAH3\_RAT ID STANDARD PRT: 831 AA.  
 AC P26433; DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE SLC9A3 OR NHE3.  
 GN Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.  
 OC OC  
 OC NCBI\_TaxID=10116;  
 OC OC  
 RN [1]  
 RP SEQUENCE FROM N.Dawley; TISSUE=Kidney;  
 RC STRAIN=Sprague-Dawley; PubMed=1577762;  
 RX MEDLINE=9250539;  
 RA Orlowski J., Kandasamy R.A., Shull G.E.;  
 RT "Molecular cloning of putative members of the Na/H exchanger gene family. cDNA cloning, deduced amino acid sequence, and mRNA tissue expression of the rat Na/H exchanger NHE-1 and two structurally related proteins." J. Biol. Chem. 267:9331-9339(1992).  
 RL -;- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS - MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANDUCTION.

-;- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -;- TISSUE SPECIFICITY: MOST ABUNDANT IN COLON AND SMALL INTESTINE, FOLLOWED BY KIDNEY AND STOMACH.

CC -;- PHOSPHORYLATED (POSSIBLE).

CC -;- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

CC -;- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.

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CC EMBL: M85300; AAA41702.1; -.  
 DR PIR: B40204; B40204;  
 DR InterPro: IPR000676; Nah\_Exchngr;  
 DR InterPro: IPR004709;  
 DR Pfam: PF00999; Na\_H\_Exchanger; 1.  
 DR PRINTS: PROL084; NAHXCHNGR;  
 DR TIGR0084; b\_cpal; 1.  
 DR Transmembrane; Glycoprotein;  
 KW Transport; TIGR00840;  
 KW Multigene family; Phosphorylation.

CC FT DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 12 25 A (M1) HYDROPHOBIC.

CC FT DOMAIN 26 51 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 52 70 B (M2) HYDROPHOBIC.

CC FT DOMAIN 71 76 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 77 96 C (M3) (POTENTIAL).  
 CC FT DOMAIN 97 109 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 110 130 D (M4) (POTENTIAL).  
 CC FT DOMAIN 131 136 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 137 157 E (M5) (POTENTIAL).  
 CC FT DOMAIN 158 177 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 178 199 F (M5A) (POTENTIAL).  
 CC FT DOMAIN 200 207 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 208 229 G (M5B) (POTENTIAL).  
 CC FT DOMAIN 230 249 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 250 271 H (M6) (POTENTIAL).  
 CC FT DOMAIN 272 287 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 288 306 I (M7) (POTENTIAL).  
 CC FT DOMAIN 307 337 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 338 359 J (M8) (POTENTIAL).  
 CC FT TRANSMEM 360 366 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 367 387 K (M9) (POTENTIAL).  
 CC FT DOMAIN 388 402 EXTRACELLULAR (POTENTIAL).  
 CC L, HYDROPHOBIC.

CC FT DOMAIN 403 423 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 424 432 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 433 453 M (M10) (POTENTIAL).  
 CC FT CARBOHYD 323 454 CYTOPLASMIC (POTENTIAL).  
 CC SEQUENCE 831 AA; 93105 MW; 774ABF10DFF99E3F CRC64;

Query Match 17.7%; Score 480.5; DB 1; Length 831;  
 Best Local Similarity 28.6%; Pred No. 3.8e-24;  
 Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;

Qy 22 VVSNLFYVALSLCACTV-LGHLLLEENRKYNESTALIIGLCTGVVTLMMTKGSSHL -FV 78  
 Db 54 IIAILWIVASLAKIVEHLSH -- KVTSVTPESAAVLIGLVLAGIV --- WAADHIAST 106  
 Qy 79 FSEDLFFTYLLPLPPIENAGFQYKKKQFFRNFMITLFGAVGMISFTTISAAIAIFSRM 138  
 Db 107 LPLTFPFYLLPLPTIVDAGYMPNRLFPGNLGTLLAYVIIWNAAATTGSLSYGFPLSG 166  
 Qy 139 NIGTLDVG - DFLAIGAIFSATDSVCFQLVNO - DTFPLFLSVLVEGGVVNDATSIYLFN 195  
 Db 167 LMGELKGIGLDEFLFGSIIIAVDPVAVLAFFEEHVNEVLIVFGESLNDADTVVLYN 226  
 Qy 196 ALQNFDELVHIDAAV -- -VLFKLFGNPFYLFLSSSTFLGV -FAGLSSAYLIKKLYIGRHSTD R 251  
 Db 227 VFEFSVTLLGGDAVTGVDCKVGIVSFFVVSLSGGTLLVEVIAFLS -- LVTR -FTKVRII 282  
 Qy 252 EVAFLMMIIMAYLSMLAFLLDLSGLITVFFCGIVMSHYTWNNVTESSRVTTKAHFATLSFI 311  
 Db 283 EPGFVFVTSYLSYLSYLSYLSMISLAAITCQCCQCYKVNQISEQATVRYTMKMLASG 342  
 Qy 312 AETFLFLYVGMDALDLEKWEASDRDGKSIGISSILGLVLIG -- RAAFVPLPSLTSNL T 369  
 Db 343 AETIIFMFLGISAVIDPVITWV ----- NTAFLVLTLYVISVRAIGVVLQQTWLNRV 393  
 Qy 370 KKPANEKITIWROQVVIWAGLIMGRGAVSIALAYNKFKTRSGHTIQLHGNAIMITSTITVVLFS 429  
 Db 394 RMVQLETI -- DQVNSYGGL -RGAVAYALV -- -VLLDEKKVKVEKKNLVFTSSTLIVVFFT 445  
 Qy 430 TMVFGMTKPKLIRLPLASGPVTPSSPSSPLSH --- SPLTSMQGSDLESTTNIVRPS 485  
 Db 446 VIFQGUTIKPLVQWLKVKRSE -- QREPKLNKLGRAFDHILSAIEDISQIGHNYLRDK 503  
 Qy 486 SLRMLLTKPHTVHYWKRFED -- -DALMR 511  
 Db 504 ----- WSNFRKFLSKVLMR 518

## RESULT 9

NAH2\_HUMAN STANDARD; PRT; 812 AA.  
 ID NAH2\_HUMAN  
 AC Q9UBY0;  
 DT 16-OCT-2001 (Rel: 40, Created)  
 DT 15-JUN-2002 (Rel: 40, Last sequence update)  
 DE Sodium/hydrogen exchanger 2 (Na<sup>+</sup>/H<sup>+</sup>) exchanger 2) (NHE-2).  
 GN NHE2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 [1] RN 9606;  
 RP SEQUENCE FROM N.A.

RX MEDLINE=90375108; PubMed=1044453;

RA Ramakotai J., Dahdal R.Y., Schmidt L., Layden T.J., Dudeja P.K.,

RT "Molecular cloning, tissue distribution, and functional expression of the human Na<sup>(+)</sup>/H<sup>(+)</sup> exchanger NHE2.";

RL Am. J. Physiol. 277:G383-G390(1999).

RN [2]

RC SEQUENCE FROM N.A.

RA Hou S., Wohldmann P.

RL Submitted (APR 1999) to the EMBL/GenBank/DDBJ databases.

RT "Molecular cloning, tissue distribution, and functional expression of the human Na<sup>(+)</sup>/H<sup>(+)</sup> exchanger NHE2.";

RL Am. J. Physiol. 277:G383-G390(1999).

RA SEQUENCE FROM N.A.

RA Ramaswamy K.;

RT "Molecular cloning, tissue distribution, and functional expression of the human Na<sup>(+)</sup>/H<sup>(+)</sup> exchanger NHE2.";

RL Am. J. Physiol. 277:G383-G390(1999).

RC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE, COLON AND KIDNEY. LOWER LEVELS IN THE TESTIS, PROSTATE, OVARY, AND SMALL INTESTINE.  
 CC -!- PTM: PHOSPHORYLATED (POSSIBLE).  
 CC -!- SIMILARITY: BELONGS TO THE NA<sup>+</sup>/H<sup>+</sup> EXCHANGER FAMILY.  
 CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA<sup>+</sup>/H<sup>+</sup> EXCHANGERS VARY AMONG AUTHORS.  
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 CC -!- DR AF073299; AAD41635.1; -.  
 CC -!- DR EMBL; AC007339; AAF19248.1; -.  
 CC -!- DR GENBANK; HGNC-11072; SLC9A2.  
 CC -!- DR InterPro; IPR000676; NAH\_Exchanger.  
 CC -!- DR InterPro; IPR004709; NAH\_Exchange3.  
 CC -!- DR PRINTS; PRO0184; NAH\_EXCHNGR.  
 CC -!- DR TIGRFAMS; TIGR00840; b\_cpal; 1.  
 KW Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport; Multigene family; Phosphorylation.  
 KW Multigene family; Phosphorylation.  
 FT DOMAIN 1 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 1 A (M1) HYDROPHOBIC.  
 FT DOMAIN 34 33 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 34 79 B (M2) HYDROPHOBIC.  
 FT DOMAIN 80 100 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 101 106 C (M3) (POTENTIAL).  
 FT TRANSMEM 107 127 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 128 138 D (M4) (POTENTIAL).  
 FT TRANSMEM 139 159 E (M5) (POTENTIAL).  
 FT DOMAIN 160 168 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 169 189 F (M5A) (POTENTIAL).  
 FT DOMAIN 190 208 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 209 229 F (M5A) (POTENTIAL).  
 FT DOMAIN 230 236 G (M5B) (POTENTIAL).  
 FT TRANSMEM 237 257 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 258 277 H (M6) (POTENTIAL).  
 FT TRANSMEM 278 298 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 299 307 I (M7) (POTENTIAL).  
 FT TRANSMEM 308 328 J (M8) (POTENTIAL).  
 FT DOMAIN 329 360 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 361 381 K (M9) (POTENTIAL).  
 FT DOMAIN 382 391 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 392 412 L (M10) (POTENTIAL).  
 FT DOMAIN 413 429 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 430 450 L, HYDROPHOBIC.  
 FT TRANSMEM 451 458 M13 (POTENTIAL).  
 FT DOMAIN 459 479 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 480 812 N-LINKED (GLCNAC, -) (POTENTIAL).  
 SQ SEQUENCE 812 AA; 91519 MW; 17FER17DC383000A CRC64;

Query Match 17.6%; Score 480; DB 1; Leng 812;  
 Best Local Similarity 27.3%; Pred. No. 4e-24;  
 Matches 143; Conservative 98; Mismatches 203; Indels 80; Gaps 19;

Qy 16 TSDYAVS -- VSINLFLVALICATVGLHLEE-NRWNESITALIIGLCTGVVILLMLTRKG 71  
 Db 72 TLDYPHQVQIPPEFLYLPPPTLILLPLKPTVPLSCLLIVGLLGG1LFGVDE-  
 Qy 72 KSSHILFVSEDFLFLPTTINAGFQYKKOFFNEMTITLFGAVGMISFTTISIAA 131  
 Db 131 KSPP -AMKTDVFFYLPLPPIVLAGYFPTPPIQFNTWVAVGLWNNSIGGVNL 188  
 Qy 132 IAFESRMNIGTLDVG - DELAIGAIFSASTDVCLQLV NQDETPFLSLVFGGVVNDA 188  
 Db 189 FGICQIEAFLGLSDITLQLNLLFGSLLSIAVDPVAVLAVENHYNEQLTYLVFGESLLNDA 248

QY	189 TSVLFNALQNF-DLVHIDAAVVLKELGNFPEYLFLSSTFLGVFAGLSSAY-----I 238	FT DOMAIN 32	65
Db	249 VTVVLYNLFKSPCOMTTETIDVFAGIANFFVVGIGVILIGTFLGFIATATTTFTHNTRV 308	FT TRANSMEM 66	85
QY	239 IKKKLYIGRHSTDREVALMLMAYLSYMLAELLDSGLTVEFCGIVMSHTWHNNTESSR 298	FT TRANSMEM 86	87
Db	309 TEPLFV -----FLYLSVYTAAENMFHSIMATACATAMNYYVEENVSQSKY 356	FT TRANSMEM 88	107
QY	299 VITKHAFATLSFAETPFLFLYGMDAL-DIEKWFASDRPGKSIGISSILGLVIGRA 357	FT TRANSMEM 108	113
Db	357 TTIKYFKMMLSSVSETLIFINGVSYVKGKHEWWNA-----FVCFTLAFCLMWRAL 407	FT DOMAIN 114	133
QY	358 FVPLSLFSLSNLTKKAPNEKITWQOQVTTWAGLMRGAVASIALAY ---NKEFRSHTQLR 413	FT TRANSMEM 134	150
Db	408 GIVFVLTQINRRTIP --LTFKDFQFLAYGSL-RGATCFLAVLPAYFPR -----I 456	FT DOMAIN 151	170
QY	414 GNAIMITSTITYVLFSTMVFGMTMKPLIIRLLPASPCHPVTEPSSPKLSHSPLITSMOGS 473	FT TRANSMEM 171	186
Db	457 -KKLFTPAIVVIIWFFTGTLPFLVFLDVKRSN--KIQQAVERSEEIVYCRLEDFHVKT 512	FT TRANSMEM 187	206
QY	474 DLESTTNIVRPSSLRMLTKPHTHVVYWP---KEDDALMRPM 513	FT DOMAIN 207	226
Db	513 GIEDVCG -----HWGINFWRDKFKEDDKYLRKL 541	FT TRANSMEM 216	235
QY	514 NAA3_DIDMA STANDARD; PRT; 839 AA.	FT DOMAIN 236	235
Db	Q28362; (Rel. 35, Created)	FT TRANSMEM 236	235
DT	01-NOV-1997 (Rel. 35, last sequence update)	FT TRANSMEM 236	235
DT	01-NOV-1997 (Rel. 35, last annotation update)	FT TRANSMEM 236	235
DT	01-JUN-2002 (Rel. 41, last annotation update)	FT TRANSMEM 236	235
GN	Sodium/Hydrogen exchanger 3 (Na(+)/H(+)) exchanger 3 (NHE-3).	FT DOMAIN 367	370
OS	Didelphis marsupialis Virginiana (North American opossum).	FT TRANSMEM 373	392
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT DOMAIN 393	442	
OC	Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.	FT CARBOHYD 443	462
OX	NCBI_TaxID=9267; [1]	FT CARBOHYD 463	481
RN	SEQUENCE FROM N.A. MOLDBASE ID: 53538256; PubMed=7631739; PMID=7631739; (Rel. 35, Last sequence update)	FT SEQUENCE 480	480
RX	Amemiya M., Yamaji Y., Cano A., Moer O. W., Alpern R. J.; DE Sodium/Hydrogen exchanger 3 (Na(+)/H(+)) exchanger 3 (NHE-3).	FT SEQUENCE 480	480
RT	Acid incubation increases NHE-3 mRNA abundance in OKP cells.";	FT SEQUENCE 480	480
RL	J. Physiol. 265:C126-C132 (1975).	FT SEQUENCE 480	480
CC	-1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION.	FT SEQUENCE 480	480
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.	FT SEQUENCE 480	480
CC	-1- PTM: PHOSPHORYLATED (POSSIBLE).	FT SEQUENCE 480	480
CC	-1- SIMILARITY: BELONGS TO THE Na(+) / H(+) EXCHANGER FAMILY.	FT SEQUENCE 480	480
CC	-1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE Na(+) / H(+) EXCHANGERS VARY AMONG AUTHORS.	FT SEQUENCE 480	480
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	FT SEQUENCE 480	480
CC	EMBL: L42522; AAA98816_1; -.	FT SEQUENCE 480	480
DR	InterPro: IPR000676; NAH_Exchngr.	FT SEQUENCE 480	480
DR	InterPro: IPR004709; NAH_Exchngr_3.	FT SEQUENCE 480	480
DR	Pfam: PF00999; Na_H_Exchngr_1.	FT SEQUENCE 480	480
DR	PRINTS; PRO184; NAH_Exchngr.	FT SEQUENCE 480	480
DR	TIGRFAMS: TIGR00840; b_cpa1; 1.	FT SEQUENCE 480	480
KW	Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport.	FT SEQUENCE 480	480
KW	Multigene family; Phosphorylation.	FT SEQUENCE 480	480
FT	DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).	FT SEQUENCE 480	480
FT	TRANSMEM 14 31 M1 (POTENTIAL).	FT SEQUENCE 480	480
RESULT 11			
NAH3_DIDMA			
ID NAH3_DIDMA			
STANDARD;			
PRT; 839 AA.			
AC Q28362;			
DT 01-NOV-1997 (Rel. 35, Created)			
DT 01-NOV-1997 (Rel. 35, last sequence update)			
DT 01-JUN-2002 (Rel. 41, last annotation update)			
GN SLCA3 OR NHE3.			
OS Didelphis marsupialis Virginiana (North American opossum).			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.			
OX NCBI_TaxID=9267; [1]			
RN RP			
RX			
RA			
RT			
RL			
CC	-1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- PTM: PHOSPHORYLATED (POSSIBLE).		
CC	-1- SIMILARITY: BELONGS TO THE Na(+) / H(+) EXCHANGER FAMILY.		
CC	-1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE Na(+) / H(+) EXCHANGERS VARY AMONG AUTHORS.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).		
CC	EMBL: L42522; AAA98816_1; -.		
DR	InterPro: IPR000676; NAH_Exchngr.		
DR	InterPro: IPR004709; NAH_Exchngr_3.		
DR	Pfam: PF00999; Na_H_Exchngr_1.		
DR	PRINTS; PRO184; NAH_Exchngr.		
DR	TIGRFAMS: TIGR00840; b_cpa1; 1.		
KW	Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport.		
KW	Multigene family; Phosphorylation.		
FT	DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 14 31 M1 (POTENTIAL).		
RESULT 11			
NAH2_RAT			
ID NAH2_RAT			
STANDARD;			
PRT; 813 AA.			
AC P48163; Q16434;			
AC 048163; Q16434;			
DT 01-FEB-1996 (Rel. 33, Created)			
DT 01-FEB-1996 (Rel. 33, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Sodium/hydrogen exchanger 2 (Na(+)/H(+)) exchanger 2 (NHE-2) (H7).			
DE SLC9A2 OR NHE2.			
GN Rattus norvegicus (Rat).			
OS Rattus norvegicus (Rat).			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus NCBI_TAXID=10116;	
[1]	SEQUENCE FROM N.A. (LONG ISOFORM). TISSUE- <i>Stomach</i> . MEDLINE=93280160; PubMed=7685026; Wang Z., Orlowski J., Shull G.E.; "Primary structure and functional expression of a novel gastrointestinal isoform of the rat Na/H exchanger."; Collins J.F., Honda T., Knobel S., Bulus N.M., Conary J., Dubois R., Ghishan F.K.; "Molecular cloning, sequencing, tissue distribution, and functional expression of a Na+/H <sup>+</sup> exchanger (NHE-2)."; Proc. Natl. Acad. Sci. U.S.A. 90:3938-3942(1993). [2]
[2]	SEQUENCE FROM N.A. (SHORT ISOFORM). TISSUE=Liver. MEDLINE=95129297; PubMed=8595899; Ghishan F.K., Knobel S.M., Summar M.; "Molecular cloning, sequencing, chromosomal localization, and tissue distribution of the human Na <sup>+</sup> /H <sup>+</sup> exchanger (SLC9A2)." ; Genomics 30:25-40(1995).
[3]	SEQUENCE FROM N.A. (SHORT ISOFORM). TISSUE=Liver; MEDLINE=95129297; PubMed=8595899; Ghishan F.K., Knobel S.M., Summar M.; "Molecular cloning, sequencing, chromosomal localization, and tissue distribution of the human Na <sup>+</sup> /H <sup>+</sup> exchanger (SLC9A2)." ; Genomics 30:25-40(1995).
-1-	FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE TOWARD COLONIC SODIUM GRADIENT. SEEKS TO PLAY AN IMPORTANT ROLE IN SUBCELLULAR LOCATION: Integral membrane protein.
-1-	ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A SHORT FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.
-1-	TISSUE SPECIFICITY: PREDOMINANTLY IN SMALL INTESTINE, COLON, AND STOMACH, WITH MUCH LOWER LEVELS IN SKELETAL MUSCLE, KIDNEY, BRAIN TESTIS, UTERUS, HEART, AND LUNG.
-1-	PTM: PHOSPHORYLATED (POSSIBLE).
-1-	SIMILARITY: BELONGS TO THE NA(+) / H(+) EXCHANGER FAMILY.
-1-	CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+) / H(+) EXCHANGERS VARY AMONG AUTHORS.
-1-	CAUTION: REF. 3 SEQUENCE WAS ORIGINALLY THOUGHT TO ORIGINATE FROM HUMAN.
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EMBL; L11236; AAA72350.1; -	
EMBL; L1104; AAA75406.1; -	
EMBL; S811591; AAC63180.1; -	
InterPro; IPR006716; Nail_Exchngr.	
InterPro; IPR004709; NaH_Exchang3.	
Pfam; PF00999; Na <sub>n</sub> H_Exchanger.	
PRINTS; PR01084; NAHEXCHNGR.	
TIGRFams; TIGR00840; b_cpal; 1.	
Transmembrane; Glycoprotein; Transport; Antipart; Sodium transport;	
Multigene family; Phosphorylation; Alternative splicing.	
DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).	
DOMAIN 14 34 A(M1) HYDROPHOBIC.	
DOMAIN 35 80 CYTOPLASMIC (POTENTIAL).	
DOMAIN 81 101 B(M2) HYDROPHOBIC.	
DOMAIN 102 107 CYTOPLASMIC (POTENTIAL).	
TRANSMEM 108 128 C(M3) (POTENTIAL).	
DOMAIN 129 139 EXTRACELLULAR (POTENTIAL).	
TRANSMEM 140 160 D(M4) (POTENTIAL).	
DOMAIN 161 169 CYTOPLASMIC (POTENTIAL).	

DT	15-JUN-2002 (Rel. 41, Last annotation update)	Last annotation update 1 (Na(+)/H(+) exchanger 1) (NHE-1).	
DE	Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1) (NHE-1).		
GN	SLC9A1 OR NHE1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.		
OX	NCBI_TAXID=10090;		
RN	[1]		
RP	SEQUENCE FROM N. A.		
RC	STRAIN=BALB/C;		
RA	Dewey M.J.; Bowman L. H. ;	the EMBL/GenBank/DBJ databases.	
RL	Submittted (MAR-1996) to the EMBL/GenBank/DBJ databases.		
-!-	FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION.		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-!- PTM: PHOSPHORYLATED (POSSIBLE).		
CC	-!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.		
CC	-!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.		
CC	-!- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.		
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CC	EMBL; U51112; AAA92976; 1. . .		
DR	MGI; MG1:102462; SIC9a1.		
DR	InterPro; IPR000676; Nah_Exchngr.		
DR	InterPro; IPR004799; Nah_exchang3.		
DR	Pfam; PF00999; Na_H_Exchanger; 1.		
DR	PRINTS; PRO1084; NAHEXCHNGR.		
DR	TIGRFAMS; TIGR00840; b_cpal; 1.		
KW	Multimembrane; Glycoprotein; Transport; Antipor; Sodium transport; Multigene family; Phosphorylation.		
FT	DOMAIN 1	CYTOPLASMIC (POTENTIAL),	
FT	DOMAIN 13	A (M1) HYDROPHOBIC.	
FT	DOMAIN 33	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN 106	B (M2) HYDROPHOBIC.	
FT	DOMAIN 128	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 131	C (M3) (POTENTIAL).	
FT	DOMAIN 151	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 163	D (M4) (POTENTIAL).	
FT	DOMAIN 184	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 189	E (M5) (POTENTIAL).	
FT	DOMAIN 211	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 230	F (M5A) (POTENTIAL).	
FT	DOMAIN 231	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 251	I (M7) (POTENTIAL).	
FT	DOMAIN 252	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 261	G (M5B) (POTENTIAL).	
FT	DOMAIN 283	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 302	H (M6) (POTENTIAL).	
FT	DOMAIN 323	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 337	I (M7) (POTENTIAL).	
FT	DOMAIN 358	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 389	J (M8) (POTENTIAL).	
FT	DOMAIN 411	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 417	K (M9) (POTENTIAL).	
FT	DOMAIN 439	EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN 453	L, HYDROPHOBIC.	
FT	TRANSMEM 474	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 483	M (M10) (POTENTIAL).	
FT	DOMAIN 504	CYTOPLASMIC (POTENTIAL).	
FT	CARBODY SEQUENCE 374	N-LINKED (GLCNAC, . . .) (POTENTIAL).	
SQ	820 AA;	314.67 MW;	0589C4D8DD348BE CRC64;
Query Match	17.6%	Score 479; DB 1; Length 820;	

Best Local Similarity	29.1%	Pred. No.	4.7e-24;
Matches	147;	Conservative	98;
Mismatches	202;	Indels	58;
Gaps	19;		
Qy	18 DYASY---VSTINLEVALLOCAVIGHLLLE--NRWNNESTALIGCTGVILLMTKGKS	73	
Db	99 DYPHYRTPEPIISLWLLACLMKIGHFVIPTISSPECLLVNLGGGLI---RGVG	154	
Qy	74 SHLFVSEDFLEFLYLPPITFNAGFKQVKFRNLTGAVGMISFFTIS--IAA	131	
Db	155 ETPPLQSDVFFFLPLPPIILDAFLAIGAFSATDSVCTLQLVNODE-TFLYSLVFGEGVNDATS	190	
Qy	132 IAIFSRMNIGLTGYDFELAIGAFSATDSVCTLQLVNODE-TFLYSLVFGEGVNDATS	190	
Db	215 VCLYGEQIINNGLDLFGSIISAVDPAVLAFFEIHINELHLIVGESLNDAVT	274	
Qy	191 TVLFNALQNF--DLVHTDAAVVLFKLGFNPFYLFLPSLSTEFLGVAGLSSAYIITKLYIGRH	247	
Db	275 VVLYLHFEEFASYDVGVL-SDFLFLGFL-SFFVVVALLGGVFGVYVYVIAFTSFR--FVSH	329	
Qy	248 STDREVALMMLMAYLSYMLAELLDISGLITVFFRGCLIVMSHYTWNTESSRVTKHAFAT	307	
Db	330 IRVIEPLFVFLYSYMAVLSSELFHSGIMALIASGVMPYVEANNSIKSHTTKYKFLKM	389	
Qy	367 NLTKRAPNEKTWRRQVVIWAGLGRGAVSTALAYNKETRSGHFQLQHGNAMITSFTRV	426	
Db	441 N---KFRIVKLTPKDOFIYIAGGL-RGAIAFSLGGL--LFLTAITVVI	492	
Qy	308 LSFLIAETFLFLYVGMDAL-DIEKWEFFASDRPKGSIGISSILLGIVLIGRAAFYPLSFLS	366	
Db	390 WSSVSETLIFLFLGIVSTVAGSHQWNW-----TIVISTIL--PCLIAVNLGVLTWF	440	
Qy	367 NLTKRAPNEKTWRRQVVIWAGLGRGAVSTALAYNKETRSGHFQLQHGNAMITSFTRV	426	
Db	441 N---KFRIVKLTPKDOFIYIAGGL-RGAIAFSLGGL--LFLTAITVVI	492	
Qy	427 LFSTMVFGMMTKPLIRLPLPASHGVPTSESPSKLHSPLTSMGSDLESNTNVRPSS	486	
Db	493 FFTVYQGMTRPLDIL-----AVKKQDETRESINEEHTQFDHLLTGIEDC----	542	
Qy	487 LRMLLKPTPVHYYWKRFDDALMR	511	
Db	543 -----GHGHGHHWK--DKLNK	556	

RESULT 13			
ID	NAH5_RAT	STANDARD;	
ID	NAH5_RAT	NAH5_RAT	
AC	Q9Z0X2;	Q9Z0X2;	
DT	30-MAY-2000 (Rel. 39, Created)	30-MAY-2000 (Rel. 39, Last sequence update)	
DT	30-MAY-2000 (Rel. 39, Last annotation update)	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Sodium/hydrogen exchanger 5 (Na(+)/H(+) exchanger 5) (NHE-5).	Sodium/hydrogen exchanger 5 (Na(+)/H(+) exchanger 5) (NHE-5).	
GN	Rattus norvegicus (Rat).	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus; OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus; NCBI_TaxID=10116;	
RN			
RP			
RC			
RC	Atapharita S., Park K., Melvin J.E.; Molecular cloning and functional expression of a rat Na+/H+ exchanger	Atapharita S., Park K., Melvin J.E.; Molecular cloning and functional expression of a rat Na+/H+ exchanger	
RC	"Molecular cloning and functional expression of a rat Na+/H+ exchanger"	"Molecular cloning and functional expression of a rat Na+/H+ exchanger"	
RC	(NHE5), highly expressed in brain."	(NHE5), highly expressed in brain."	
RT	J. Biol. Chem. 274:4383-4388 (1999).	J. Biol. Chem. 274:4383-4388 (1999).	
RL	-!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION (BY SIMILARITY).	-!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION (BY SIMILARITY).	
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.	-!- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	-!- PTM: PHOSPHORYLATION (POSSIBLE).	-!- PTM: PHOSPHORYLATION (POSSIBLE).	
CC	-!- SIMILARITY: BELONGS TO THE Na(+)/H(+) EXCHANGER FAMILY.	-!- SIMILARITY: BELONGS TO THE Na(+)/H(+) EXCHANGER FAMILY.	
CC	-!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.	-!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.	
CC	DOMAINS A, B AND L ARE NOT BELIEVED TO BE TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.	DOMAINS A, B AND L ARE NOT BELIEVED TO BE TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.	

Query Match

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FT DOMAIN	4.74	4.82	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	4.83	5.03	M (M10). (POTENTIAL).
FT DOMAIN	5.04	8.22	CYTOSMERIC (POTENTIAL).
FT CARBHYD	3.74	3.74	N-LINED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE	822 AA;	92003 MW;	E971ACD4EB88DAA CRC64;
Query Match Score	17.6%	Score 478;	DB 1;
Best Local Similarity	28.7%	Length 822;	
Matches 145;	Conservative 101;	Pred. No. 5.5e-24;	
	Mismatches 201;	Indels 58;	Gaps 19;
Qy 18 DYASV--VSINLFVALCILPPILFNAGFOVKKKOFFRNMFTLTFGAYGTMSFPTIS-TAA	73		
Dy 99 DYLHVRTPPFESLWLILLACLMKIGHVPIPTTIVPESCLLIVVGLGLI--KGVG 154			
Qy 74 SHLFVSEDFIYFLPLPPIFNAGFOVKKKOFFRNMFTLTFGAYGTMSFPTIS-TAA	131		
Dy 155 ETPPLQLSDVFFLFLPPIFLDAGYFLPLQFTENLTGTLIAFYVTLWNAFLGGGLYA	214		
Qy 132 IAIFSRMNTIGLWDGFDFLAGAIFATSDCTYLOVNLNOD-EPTFLYSLVFGEVVNDATIS	190		
Dy 215 VCLVGQEIQNINGLIDLTLLFGSITSAVDPAVAVFEEIHNELLHLVFSSESLLNDAVT	274		
Qy 191 IVFLNQAL--NFDLVHDAVVLRFGLNNFPYLFLSSTFLGCFAGLISAYTIKKLYIGRH	247		
Dy 275 VVYLHFEFPANYSDFGIGI-SDFIFGLFL-SFIVVALGGFVWVYGYTAFFTSR--FTSH	329		
Qy 248 STDREVALMMALMAYLSYMMLAELLDLSGLILTYFFCGIVMSHYTWHNYESSRVTTKHAFAT	307		
Dy 330 IRVIEPLFVFLYPSYMAYLSSAFLHSGIMALIASGYVMRMPEVEANISHKSHTTIKFKLW	389		
Qy 308 LSFIAETFLFLYVGMDAL-DIEKWEEADSQRGKSIGISSLLGLVIGRAAFVFPLSFLS	366		
Dy 390 WSSVSETLFLIFLGTVSTVAQSHQWN-----TFVYSTLIL-FCLJARVGVVLWTWEI	440		
Qy 367 NLTKRAPNEVLTWQOYVNWAGLMGAVSIALAYNKRTFRSHTQLHGNAIMITSITIVPSS	426		
Dy 441 N---KFRIVKTPKDOFIAYGGL-RGAIAASLGY-LMDMKHFPWCD-LFLTAITV 492			
Qy 427 LFSTMFVGMMTKPLIRLPLLPGSHPVTESESPSSPKSLHSPILTSMOGSDLESTTNIVRPPS	486		
Dy 493 FTFVQGMTRPLVDL-----AVKKQETKRSINEEHTQFLDHLTGIEDIC---	542		
Qy 487 LRMLLTKPTITYHYWKRFDDALMR 511			
Dy 543 -----GYGHGHHWIK----DKLNR 556			
RESULT 15			
NAHL_BOVIN	STANDARD;	PRT;	817 AA.
ID Q28036;			
AC Q28036;			
DT 01-NOV-1997 (Rel. 35, Created)			
DT 01-NOV-1997 (Rel. 35, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Sodium/hydrogen exchanger 1 ( $\text{Na}^+/\text{H}^+$ ) exchanger 1 (NHE-1).			
GN SLC9A1 OR NHE1.			
OS Bos taurus (Bovine).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;			
OC Bovidae; Bovinae; Bos.			
OX NCBI_TAXID=9913;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE:Heart;			
RA Zhu H., Zhang Q., Zhang X., Liu W., Trumbly R.J., Garlid K.D.,			
RA Sun X.;			
RL Submitted ('MAR-1996' to the EMBL/Genbank/DBJ databases.			
CC FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED			
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL			
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD			
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL			
CC TRANSDUCTION.			
CC - SUBCELLULAR LOCATION: Integral membrane protein.			

```

Db 326 IRVIEPLFVFLYSYMAYLSAELFHSGIMALIASGVYMRPVEANISHKSSTTIKYFLKM 385
Qy 308 LSFIAETFLFYVGMDALDIE -- KWEFASDRPGKSGISSLLGLVLIGRAAFVPLSF 364
Db 386 WSSVSETLIFLGVSTAGSHWNNTFV ----- ISPLL -- FCLIAVVLGVGLLTW 434
Qy 365 LSNLTKKAPNEKITWROQQVIIWAGLMRGAVSIALAYNKFRSGHTQLHGNAIMTSTIT 424
Db 435 FTN -- KFRITKLTPKDQFIAYGGI - RGAAFAFSGLY - LIDKKHFFPMCD - LFLLTAIT 486
Qy 425 VVLSTMWFGMTKPLTRILLIPASGHIPVTSSPSSPKSLHSPLLTSMOGSDESTTNIVRP 484
Db 487 VIFFTYFVOGHTIRPLYDLL ----- AVKKQETKRSINEEHTQFLDHLLTGIEDIC-- 538
Qy 485 SSLRMLLTkpHTVHYWRKTDALMR 511
Db 539 ----- GHYGHHHWK -- DKLNR 552

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Search completed: March 26, 2003, 18:53:06  
 Job time : 34 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2722	100.0	Q9SXJ8	535	10	Q9SXJ8	Q9sxj8 oryza sativ
2	2105.5	77.4	Q9FBN0	555	10	Q9FBN0	Q9fzn0 triplex gm
3	2103.5	77.3	Q9AH6	540	10	Q9AH6	Q94lx5 petunia hyb
4	2095.5	77.0	Q94LX4	553	10	Q94LX4	Q94lx4 niememberg
5	2080	76.4	Q9CW6	546	10	Q9CW6	Q9caw6 arabidopsis
6	2065.5	75.9	Q94E0	542	10	Q94E0	Q94ie0 ipomoea tri
7	2055.5	75.5	Q9FB3	542	10	Q9FB3	Q9feb3 pharbitis n
8	2054.5	75.5	Q94E25	556	10	Q94E25	Q94k25 suada mari
9	2043	75.1	Q9AH6	542	10	Q9AH6	Q9arh6 citrus para
10	2023.5	74.3	Q9PK3	538	10	Q9PK3	Q9zpk3 arabidopsis
11	1966	72.2	Q94LX3	555	10	Q94LX3	Q94lx3 torenia hyb
12	1931	70.9	Q9SD0	552	10	Q9SD0	Q9sq0 arabidopsis
13	1921.5	70.6	Q9RM4	546	10	Q9RM4	Q94bm4 triticum ae
14	1879	69.0	Q93FH2	534	10	Q93FH2	Q93yh2 lycopersico
15	1698.5	62.4	Q94E55	457	10	Q94E55	Q04655 arabidopsis
16	1529	56.2	Q9U624	529	10	Q9U624	Q9u624 drosophila
			Q9vN99	295	10	Q94bm3	Q94bm3 triticum ae
			Q9XZH4	576	11	Q9RAD1	Q9rad1 mus musculus
			Q9VPJ1	561	5	Q9XZH4	Q9xzh4 drosophila
			Q9S2X8	649	5	Q9VPJ1	Q9vpj1 drosophila
			Q9T5R7	649	5	Q9S2X8	Q9sxx8 drosophila
			Q9T5R8	611	5	Q9T5R7	Q9t5r7 caenorhabditis
			Q9T5R8	630	5	Q9T5R8	Q9t5r8 caenorhabditis
			Q9U624	687	5	Q9U624	Q9u624 drosophila
			Q9V44	629	5	Q9U624	Q9v44 caenorhabditis
			Q9V99	727	5	Q9V5R3	Q9v99 drosophila
			Q9V5R3	655	5	Q9T5R3	Q9v5r3 caenorhabditis
			Q9T5R4	681	5	Q9T5R4	Q9t5r4 caenorhabditis
			Q9XW14	703	5	Q9XW14	Q9xw14 caenorhabditis
			Q96396	517	10	Q96396	Q96396 arabidopsis
			Q96183	505	10	Q96183	Q96183 homo sapien
			Q913726	725	4	Q96T83	Q913726 schizosaccharomyces pombe
			Q91726	569	3	Q91726	Q91726 lycopersicon esculentum
			Q93YH1	531	10	Q93YH1	Q93YH1 arabidopsis
			Q983395	525	10	Q983395	Q983395 mesembryanthemum crystallinum
			Q91KH5	140	10	Q91KH5	Q91KH5 mesembryanthemum crystallinum
			Q9LKHS	153	10	Q9LKHS	Q9LKHS mesembryanthemum crystallinum
			Q96T83	553	20..3	Q96T83	Q96T83 zea mays (mexican corn)
			Q9ATZ9	569	3	Q9ATZ9	Q9ATZ9 homo sapien
			Q9Y507	437	4	Q9Y507	Q9y507 pneumocystis carinii
			Q9HEX3	560	3	Q9HEX3	Q9hex3 drosophila melanogaster
			Q9V1F9	518	5	Q9V1F9	Q9v1f9 drosophila melanogaster
			Q9WP4	582	5	Q9WP4	Q9wp4 drosophila melanogaster
			Q9NGZ4	1203	5	Q9NGZ4	Q9ngz4 drosophila melanogaster
			Q9NCQ0	1179	5	Q9NCQ0	Q9ncq0 aedes aegypti

Db	61 TGVVILIMTKSSHLFVSSDLFFYLLPPIFNAGFOVKKKQFRNFMNTITLEGAVT	120	Qy	127 ISIAIAIAIFSRMNGITDVGDELAIGAIFSAIDSVCILQLVNQDETFLFYLISLVFGCWWN	186	
Oy	121 MISFFTISIAIAIFSRMNGITDVGDFLATAIGATISATSDVCILQLVNQDETFLFYLISLVF	180	Db	129 ISLGALSIFFKLIDIGTLELADYLAIGAIFAAIDSVCILQLVNQDETFLFYLISLVFGCWWN	188	
Db	121 MISFFTISIAIAIFSRMNGITDVGDFLATAIGATISATSDVCILQLVNQDETFLFYLISLVF	180	Qy	187 DATSIVLFNALQNFDLVHDAAVVLFAGLNFYLLSSTFLGVFAGLSSAYIJK	246	
Oy	181 GEGVNDATSVLFLNALQNFDLVHDAAVVLFAGLNFYLLSSTFLGVFAGLSSAYIJK	240	Db	189 DATSVLFLNALQSFDFLRIDHRIALQMGNFNLFTASLTLGAFGTGELSAYIJKYFG	248	
Db	181 GEGVNDATSVLFLNALQNFDLVHDAAVVLFAGLNFYLLSSTFLGVFAGLSSAYIJK	240	Qy	187 DATSIVLFNALQNFDLVHDAAVVLFAGLNFYLLSSTFLGVFAGLSSAYIJK	246	
Oy	241 KLYIGRHSTDREVALMLMAYLSYMLAELLSGLSLTVPFGTVMSHYTWHNVTESRSVT	300	Db	249 HSTDREVALMLMAYLSYMLAELFLYLSGLTVPFGTVMSHYTWHNVTESRSVTKHAF	308	
Db	241 KLYIGRHSTDREVALMLMAYLSYMLAELLSGLSLTVPFGTVMSHYTWHNVTESRSVT	300	Qy	307 TLSFLATEFLFLYLVGMDALDIKEWPAEPRGKSIGISSLLGLYLGRAFVEPLSFLS	366	
Oy	301 TKHAPNEKLTWRCOYVIWAGLMRGAVSTALAYNKTRSGHTOLHGNAIMT	420	Db	309 TLSFVAEVFLFLYVGMDALDIKEWKRFVSDSGTISAVSSILLGLYLGRAFVFPLSFLW	368	
Db	301 TKHAPATLSETAEFLFLYVGMDALDIKEWKRFVSDSGTISAVSSILLGLYLGRAFVF	420	Qy	367 NLTKAPNEKLTWRCOYVIWAGLMRGAVSTALAYNKTRSGHTOLHGNAIMTSTTVY	426	
Oy	361 PLSFLSNLTKAPNEKLTWRCOYVIWAGLMRGAVSTALAYNKTRSGHTOLHGNAIMT	420	Db	369 NFAKSQSSEKTFENQOIVIWAGLMEGAVSMALAYNQTRSGHTOLHGNAIMTSTSVV	428	
Db	361 PLSFLSNLTKAPNEKLTWRCOYVIWAGLMRGAVSTALAYNKTRSGHTOLHGNAIMT	420	Qy	427 LFSTMVFGMMTKPLRLLPASGH-- -PVTESEPPSKPSLHSPLTSMSQDSL	475	
Oy	421 STIVYLFSTMVFGMMTKPLRLLPASGHVSEPPSPSKLSHSPLTSMSQDSLESTIN	480	Db	429 LFSTMVFGLJTKPLRLLPQPKHETCSCTVSDYGSKPSLPLBEGNQYEVDGNGNH	488	
Db	421 STIVYLFSTMVFGMMTKPLRLLPASGHVSEPPSPSKLSHSPLTSMSQDSLESTIN	480	Qy	476 ESTT-- -NIVRPSLRLMLLTKPHTHVYWKFDALMRPMFGRGVPPSPGSPTEQS	531	
Oy	481 IVRPSLRLMLLTKPHTHVYWKFDALMRPMFGRGVPPSPGSPTEQS	535	Db	489 EDTTPRTIVRPSLRLMLNAPHTVHYWKFDALMRPMFGRGVPPSPGSPTEQS	547	
Db	481 IVRPSLRLMLLTKPHTHVYWKFDALMRPMFGRGVPPSPGSPTEQS	535	RESULT 3			
Q94LY5						Q94LY5
ID	Q94LY5		PRT:	PRELIMINARY:	PRT:	540 AA.
AC	Q94LY5;					
DT	01-DEC-2001 (TREMBLrel. 19, Created)					
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)					
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)					
DE	Na/H_antiporter_Nhx1.					
GN	AGNIXII.					
OS	Atriplex_gmelini.					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
OC	Asparagales; euasterids I; Solanales; Solanaceae; Petunia.					
OX	NCBI_TaxID=4102;					
RN	[1]					
RA	SEQUENCE FROM N.A.					
RA	RT "Plant Na-H antiporter";					
RA	RT Submitted (Nov-2000) to the EMBL/GenBank/DBJ databases.					
RA	DR EMBL: AB051817; BA56105; 1.					
RA	DR InterPro: IPR001179; FKBP_PPIase.					
RT	DR InterPro: IPR000676; Na_H_Exchanger.					
RT	DR PROSITE: PS00453; FKBP_PPIASE_1; UNKNOWN_1.					
RT	DR PROSITE: PS00453; FKBP_PPIASE_1; UNKNOWN_1.					
RT	DR SEQUENCE: 540 AA; 59510 MW; BCE2740F275E896A CRC64;					
Query Match						Score 2103.5; Length 540;
Matches	404; Conservatve 53; Mismatches 62; Indels 3; Gaps 1;					
Qy	15 TTSDYASVVSINLEVALCIVLGHLEENRWNESTALIGLCTGVILLMTKGKSS	74	Qy	75 HLIVFSEDLFFYLLPPIFLNAGFOVKKKOFFERNFTITLEFGAVGTMISFTTISIAIAI	134	
Db	16 STSDHQSVVSINLEVALCIVLGHLEENRWNESTALIGLCTGVILLMTKGKSS	75	Db	76 HLIVFSEDLFFYLLPPIFLNAGFOVKKKOFFERNFTITLEFGALGTLSLSPITISLGA	135	
Qy	7 ARIALGALTTSYASVVSINLEVALCIVLGHLEENRWNESTALIGLCTGVILL	66	Qy	135 FSRMNGITDVGDFLAIQAIISATDSVCILQLVNQDETFLFYLISLVFGCWWN	194	
Db	10 SGMDAL-TSDHASVSMNLFVALCCGTCIVLGHLEENRWNESTALIGLCTGVILL	68	Db	136 FKRKNIGGSEIGDYLAIQAIISATDSVCILQLVNQDETFLFYLISLVFGCWWN	195	
Qy	67 LMTKGKSSHLFVSEDLFFYLLPPIFNAGFOVKKKOFFERNFTITLEFGAVGTMISFT	126	Db	137 FKRKNIGGSEIGDYLAIQAIISATDSVCILQLVNQDETFLFYLISLVFGCWWN	195	
Db	69 LITGGKSSHLFVSEDLFFYLLPPIFNAGFOVKKKOFFERNFTITLEFGAVTLYSFTI	128	Qy	195 NALQNFDDLVHDAAVVLFAGLNFYLLSSTFLGVFAGLSSAYIJKLYIGRHSTDREVA	254	

Db	196	NAIQNFDLSDHIDTGKAMELVGNFLYFAASSTALGVAAGILSAYIJKLYFGRISTDREVA	255	:          :	Db	256	TMILMAYLSYMLAELFLY.SYMLAELFLY.SGIL.TVFCSTIVMSHTWHNTVTESSRTTKHTFATLSFAEI	315
Qy	255	LMMILMAYLSYMLAELFLSGILTVEFGTIVMSHTWHNTVTESSRTTKHTFATLSFAIT	314	:	Qy	315	FLFLYGMALDIEKWEFASDRPGKSIGISLLGLVLIGRAAFVPLFSNLTKKAPN	374
Db	256	IMILMAYLSYMLAELFLSGILTVEFGTIVMSHTWHNTVTESSRTTKHTFATLSFAIE	315	:	Db	316	FLFLYGMALDIEKWKVPSDGTTSKVSILLGLVYGRGAFFPLFSNLTKKNPE	375
Qy	315	FLFLYGMALDIEKWEFASDRPGKSIGISLLGLVLIGRAAFVPLFSNLTKKAPN	374	:	Qy	375	EKITWROQQVVIWAGLMRGAVSIALAYNKSTRSGTOLQHNAIMITSTTVLFSTMVFG	434
Db	316	FLFLYGMALDIEKWKVPSDGTTSKVSILLGLVYGRGAFFPLFSNLTKKTF	375	:	Db	376	DKTSFNQOVTIWAGLMRGAVSIALAYNQFTRGHTQLRANAIMITSTTVLFSTMVFG	435
Qy	375	EKITWROQQVVIWAGLMRGAVSIALAYNKSTRSGTOLQHNAIMITSTTVLFSTMVFG	434	:	Qy	435	MMTKLPLRLLLPSASH--PVTSEPPSSPKSLHSPLTSMQGSDLESTTNVRPSSLRMLL	491
Db	376	AKISFNOQVTIWAGLMRGAVSIALAYNQFTRGHTQLRANAIMITSTTVLFSTMVFG	435	:	Db	436	LMTKLPLRLLLPSQHLRMLMISSPMTPKSFIVPLDSTDQSEADLRHVRPHSLRMLL	495
Qy	435	MMTKLPLRLLLPSASH--PVTSEPPSSPKSLHSPLTSMQGSDLESTTNVRPSSLRMLL	491	:	Qy	492	TKPTHTVHYWYWRKFEDDALMRPMGGRGVPFESGSPTE	529
Db	436	LMTKLPLRLLLPSKHLRMLMISSPMTPKSFIVPLDSTDQSEADLRHVRPHSLRMLL	495	:	Db	496	STPSHTVHYWYWRKFEDNAFMRPVFCGGFVFPVFGSPTE	533
Qy	492	TKPTHTVHYWYWRKFDDALMRPMGGRGVPFESGSPTEQSHG	533	:				
Db	496	STPSHTVHYWYWRKFDDALMRPMGGRGVPFESGSPTEQSHG	537	:				
					RESULT 5			
				Q9CAW6	PRELIMINARY;	PRT:	546 AA.	
				ID	Q9CAW6			
				AC	Q9CAW6;			
				DT	01-JUN-2001	(TREMBlrel. 17, Created)		
				DT	01-JUN-2001	(TREMBlrel. 17, Last sequence update)		
				DT	01-JUN-2002	(TREMBlrel. 21, Last annotation update)		
				DE	Putative sodium proton exchanger (Na+/H+ exchanger 2).			
				GN	I9J14_2 OR NHX2.			
				OS	Arabidopsis thaliana (Mouse-ear cress).			
				OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
				OC	Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;			
				OC	eurosid II; Brassicaceae; Arabidopsis.			
				NCBI_TAXID	=3702;			
				OX	Jordan N., Bangert S.,			
				RN	[1]			
				RP	SEQUENCE FROM N.A.			
				RC	SEQUENCE FROM N.A.			
				RC	SEQUENCE FROM COLUMBIA;			
				RC	MEIDLINE=21016720; PubMed=11130713;			
				RA	Fartmann B., Valle G., Bloecker H., Rieger M., Ansorge W., Unseld M., Obermaier B.,			
				RA	Delseny M., Boutry M., Grivell L.A., Maché R., Puigdomenech P.,			
				RA	De Simone V., Choisne N., Artigueau F., Robert C., Brottier P.,			
				RA	Wincher P., Cattolico L., Weissbach J., Saurin W., Quetier F.,			
				RA	Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,			
				RA	Wurmbach E., Drzonek H., Erflie H., Holland R., Brandt P., Nyakatura G.,			
				RA	Viedemann R., Kranz H., Voss H., Toppo S., Simionati B.,			
				RA	Vezzi A., D'Angelio M., Pallavicini A., Toppo S., Simionati B.,			
				RA	Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordstek G.,			
				RA	Reichelth J., Schartel C., Perez-Perez A., Terol J., Clement J.,			
				RA	Navarro P., Collado C., Perez-Perez A., Ottewaelder B., Duchemin D.,			
				RA	Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Nasuy D.,			
				RA	Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Catracubert E.,			
				RA	Monfort A., Argirion A., Flores M., Liquori R., Vitale D.,			
				RA	Mannhaupt G., Haase D., Schoof H., Rudd S., Zuccaria P., Newes H.-W.,			
				RA	Mayer K.F.X., Kaul S., Town C., Koo H.-L., Tally L.J., Jenkins J.,			
				RA	Rooney T., Rizzo M., Walls A., Utterback T., Fujii C.Y., Shea T.P.,			
				RA	Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,			
				RA	Paeuss D., Mittscher J., Sellers P., Gill J.E., Feldblyum T.V.,			
				RA	Argirion A., Flores M., Liquori R., Vitale D.,			
				RA	Mannhaupt G., Haase D., Schoof H., Rudd S., Zuccaria P., Newes H.-W.,			
				RA	Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,			
				RA	Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,			
				RA	Kiyotawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,			
				RA	Nakayama S., Nakazaki N., Shimpou S., Takeuchi C., Wada T.,			
				RA	Watanahe A., Yamada M., Yasuda M., Tabata S., Thaliana.			
				RT	"Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana."			
				RL	Nature 408:820-822(2000).			
				RN	[2]			
				RP	SEQUENCE FROM N.A.			
				RA	Yokoi S., Quintero F.J., Cubero B., Ruiz T., Bressan R.A.,			
				RA	Hasegawa P.M., Pardo J.M.;			
				RT	"Differential expression and function of Arabidopsis thaliana NHX Na+/H+ antiporters in the salt stress response."			
				RT				

RL	Plant J. 0:0-0(2002).	Plant Cell Physiol. 42:451-461 (2001).
DR	AC09465; AAGJ1408_1; -.	EMBL; AB154979; BAB60901_1; -.
EMBL	AF490586; AAM08403_1; -.	DR
DR	IPR001179; FKBP_PPase.	InterPro; IPR001179; FKBP_PPase.
DR	IPR004709; Nah_Exchang3.	InterPro; IPR004709; Nah_Exchang3.
DR	IPR000675; Nah_Exchanger_1.	InterPro; IPR000675; Nah_Exchanger_1.
Pfam	PF00999; Na_H_Exchanger_1.	Pfam; PF00999; Na_H_Exchanger_1.
PRINTS	PRO1084; NAHEXCINGR.	PRINTS; PRO1084; NAHEXCINGR.
TIGRFAMS	TIGR00840; b_cpal_1.	TIGRFAMS; TIGR00840; b_cpal_1.
PROSITE	PS00453; FKBP_PPase_1; UNKNOWN_1.	PROSITE; PS00453; FKBP_PPase_1; UNKNOWN_1.
SEQUENCE	546 AA; 60522 MW; BEA270D40446360B CRC64;	SEQUENCE 542 AA; 60024 MW; 0C381CFE78B239C CRC64;
SO		
Query Match	75.9%; Score 2065.5; DB 10; Length 542;	Query Match 75.9%; Score 2065.5; DB 10; Length 542;
Best Local Similarity	76.6%; Pred. No. 2e-144;	Best Local Similarity 76.6%; Pred. No. 2e-144;
Matches	402; Conservative 50; Mismatches 64; Gaps 9; Caps 3;	Matches 402; Conservative 50; Mismatches 64; Gaps 9; Caps 3;
Qy		
15	TTSDAYSVSINLFLVALCACIVGHLLBEENRWNESITALLIGCTGYVILLMTKGSS 74	Qy
15	STSDHASVVSINLFLVALCACIVGHLLBEENRWNESITALLIGCTGYVILLSRGKNS 74	Db
75	HLYFVYSEDLFFIYLPPPLIFNAGFQVKKKOFFERNFTMITLEFGAVTGMISFFTISAAIA 134	Qy
75	HLYFVYSEDLFFIYLPPPLIFNAGFQVKKKOFFERNFTMITLEFGAVTGMISFFTISAAIA 134	Db
75	HLYFVYSEDLFFIYLPPPLIFNAGFQVKKKOFFERNFTMITLEFGAVTGMISFFTISAAIA 134	Qy
135	FSMNNIGLTDVGDELAIGAIFSAATDSVCLQLNQDETFLYSLVFGVVNDATSVLF 194	Qy
135	FKDGTDGFGLFLGAIAFAATDSVCLQLNQDETFLYSLVFGVVNDATSVLF 194	Db
195	NALONFLDVHIDAAVVLKFLNQDETFLYSLVFGVVNDATSVLF 254	Qy
195	NAIQSDFLTHNEAFAOFLGNFYFLSSTFLGVAGTLGAGTGLKLYFGRHSTDREVA 254	Db
255	LMMMLAYLSYMLAELLDLSGLTVEFCGIVMSHYTWHNYTESSRVTTKHAFAFLSFAET 314	Qy
255	LMMMLAYLSYMLAELDFLGSILTVFECGIVMSHYTWHNYTESSRVTTKHAFAFLSFAET 314	Db
315	FFLFLYGMDALDEKWEFASDRPKSIGISSITLGVLGRAAFVPLSFLSNLTKKAPNC 374	Qy
315	FFLFLYGMDALDEKWEFASDRPKSIGISSITLGVLGRAAFVPLSFLSNLTKKAPNC 374	Db
375	EKTWROQVVIWAGLMRGAVSIALAYNKFTSGHTOLGNAMITSTITVVLFSTMVFG 435	Qy
375	EKTWROQVVIWAGLMRGAVSIALAYNKFTSGHTOLGNAMITSTITVVLFSTMVFG 435	Db
375	EKISIKQOVVIWAGLMRGAVSIALAYNKFTSGHTOLGNAMITSTITVVLFSTMVFG 434	Qy
435	MNTKPLIRLLP --- ASGHPyTSEPPSPKSKLHSPLTSMSQGSDLE --- STINVRPSS 486	Db
435	MNTKPLIRLYMPHQKATSTSMSLSDDTPSKTHPLDGEQLDSELPGSHQDVPRTS 494	Qy
487	LRMLLTTRPTHTHYWWRKFDALMRPMFGRGRGVFPSPGSPTEQS 531	Db
495	LRGFLMRPRTPTHYWWQFDAFMRPVFGGRGFVFPVFGSPSPTEQS 540	Db
RESULT 6		
994IE0	PRELIMINARY; PRT; 542 AA.	RESULT 6
ID	994IE0	994IE0
AC		PRELIMINARY; PRT; 542 AA.
DT	09FEB 3, 2001 (TRIMBLrel. 16, Created)	DT 09FEB 3, PRELIMINARY; PRT; 542 AA.
IC	01-MAR-2001 (TRIMBLrel. 16, Last sequence update)	IC 01-MAR-2001 (TRIMBLrel. 16, Created)
DT	01-DEC-2001 (TRIMBLrel. 19, Last sequence update)	DT 01-MAR-2001 (TRIMBLrel. 16, Last sequence update)
DT	01-DEC-2002 (TRIMBLrel. 19, Last annotation update)	DT 01-JUN-2002 (TRIMBLrel. 21, Last annotation update)
DT	01-JUN-2002 (TRIMBLrel. 21, Last annotation update)	DE Na+/H+ exchanger (Na+/H+ exchanger protein).
DE	DE Na+/H+ exchanger.	DE Na+/H+ exchanger (Na+/H+ exchanger protein).
GN	GN Phorbol ester (Violet).	GN Phorbol ester (Violet).
OC	OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;	OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
CC	CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC	CC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.	CC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
OX	OX NCBI_TaxID:35884;	OX NCBI_TaxID:35884;
RN	[1]	RN [1]
RP	RP SEQUENCE FROM N_A.	RP SEQUENCE FROM N_A.
RC	RC STRAIN=KK2SK-2; TISSUE=LEAF, AND FULLY COLORED FLOWER BUDS;	RC STRAIN=KK2SK-2; TISSUE=LEAF, AND FULLY COLORED FLOWER BUDS;
RX	RX MEDLINE=21276661; PubMed=11382810;	RX MEDLINE=20487008; PubMed=10103495;
RA	RA Yamaguchi T.; Fukada-Tanaka S.; Inagaki Y.; Saito N.; Iida S.;	RA Fukada-Tanaka S.; Inagaki Y.; Yamaguchi T.; Saito N.; Iida S.;
RT	RT "Colour-enhancing protein in blue petals."	RT "Colour-enhancing protein in blue petals."
RL	RL Yoneuchi-Sakakibara K.; Tanaka Y.; Kusumoto T.; Iida S.;	RL Nature 407:581-581(2000).
IT	IT Genes Encoding the vacuolar Na+/H+ Exchanger and Flower Coloration."	IT

RP	SEQUENCE FROM N.A.	RN [1]	SEQUENCE FROM N.A.
RC	STRAIN=PR-R; TISSUE="LEAF";	RP	SEQUENCE FROM N.A.
RX	MEDLINE=2127666; PubMed=11382810;	RA Zhang H.; Zhang Q.; Ma X.;	RA Zhang H.; Zhang Q.; Ma X.;
RA	"Na <sup>+</sup> /H <sup>+</sup> antiporter in <i>Suaeda salsa</i> ."	RT "Na <sup>+</sup> /H <sup>+</sup> antiporter in <i>Suaeda salsa</i> ."	RT "Na <sup>+</sup> /H <sup>+</sup> antiporter in <i>Suaeda salsa</i> ."
RA	Yamaguchi T., Fukada-Tanaka S., Inagaki Y., Saito N.,	RL Submitted (APR 2001) to the EMBL/GenBank/DBJ databases.	RL Submitted (APR 2001) to the EMBL/GenBank/DBJ databases.
RA	Yonekura-Sakakibara K, Tanaka Y., Kusumi T., Iida S., "Genes Encoding the vacuolar Na <sup>+</sup> /H <sup>+</sup> Exchanger and Flower Coloration,"	DR EMBL; AF370358; AAC53432; 1-	DR EMBL; AF370358; AAC53432; 1-
RT	Plant Cell Physiol. 42:451-461 (2001).	DR InterPro; IPR001179; FKBPP_Ptase.	DR InterPro; IPR001179; FKBPP_Ptase.
RL		DR InterPro; IPR004709; Na <sup>+</sup> _Exchang3.	DR InterPro; IPR004709; Na <sup>+</sup> _Exchang3.
DR	EMBL; AB031990; BAB16381; -	DR IPN00616; Na <sup>+</sup> _Exchng1.	DR IPN00616; Na <sup>+</sup> _Exchng1.
DR	EMBL; AB03199; BAB10501; -	DR Pfam; PF00999; Na <sup>+</sup> _Exchanger; 1.	DR Pfam; PF00999; Na <sup>+</sup> _Exchanger; 1.
DR	EMBL; AB055062; BAB60899; -	DR TIGRFAMS; TIGR00840; b_cpa1; 1.	DR TIGRFAMS; TIGR00840; b_cpa1; 1.
DR	InterPro; IPR001179; FKBPP_Ptase.	DR PROSITE; PS00453; FKBPP_Ptase_1; UNKNOWN_1	DR PROSITE; PS00453; FKBPP_Ptase_1; UNKNOWN_1
DR	InterPro; IPR004709; Na <sup>+</sup> _Exchang3.	DR PROSITE; PS00453; FKBPP_Ptase_1; UNKNOWN_1	DR PROSITE; PS00453; FKBPP_Ptase_1; UNKNOWN_1
DR	InterPro; IPR000676; Na <sup>+</sup> _Exchng1.	DR SEQUENCE 556 AA; 61672 MW; DDF6AB96647D48E CRC64;	DR SEQUENCE 556 AA; 61672 MW; DDF6AB96647D48E CRC64;
DR	PRINTS; PRO1084; NAHPCXCHNGP.		
DR	TIGRFAMS; TIGR00840; b_cpa1; 1.		
DR	PROSITE; PS00453; FKBPP_Ptase_1; UNKNOWN_1.		
SQ	SEQUENCE 542 AA; 59973 MW;	Query Match 75.5%; Score 2055.5; DB 10; Length 556;	Query Match 75.5%; Score 2054.5; DB 10; Length 556;
		Best Local Similarity 74.2%; Pred. No. 1.1e-143;	Best Local Similarity 74.2%; Pred. No. 1.1e-143;
		Matches 395; Conservative 56; Mismatches 68; Gaps 2;	Matches 395; Conservative 56; Mismatches 68; Gaps 2;
Qy	16 TSDYASVSVINLFVALCACIVGHILEENRWVNESITALIIGLCTGVVLLMTKGSH 75	Qy 13 LYTTSDYASVSVTSINLFVALCACIVGHILEENRWVNESITALIIGLCTGVVLLMTKGK 72	Qy 13 LYTTSDYASVSVTSINLFVALCACIVGHILEENRWVNESITALIIGLCTGVVLLMTKGK 72
Db	16 TSDHASVVSMLFVALCACIVGHILEENRWVNESITALIIGLCTGVVLLMTKGSH 75	Db 15 MVSSPSDHASVVSMLFVALCACIVGHILEENRWVNESITALIIGLCTGVVLLMTKGK 74	Db 15 MVSSPSDHASVVSMLFVALCACIVGHILEENRWVNESITALIIGLCTGVVLLMTKGK 74
Qy	76 LFFVSEDDLFIFYLPLPIIFNAGPQVKKQFFRNFMITLGAVGTMISFFTISTATAIAF 135	Qy 73 SSHLFVSEDLFFFLPYLPLPIIFNAGPQVKKQFFRNFMITLGAVGTMISFFTISTAAI 132	Qy 73 SSHLFVSEDLFFFLPYLPLPIIFNAGPQVKKQFFRNFMITLGAVGTMISFFTISTAAI 132
Db	76 LLYVSEDDLFIFYLPLPIIFNAGPQVKKQFFRNFMITLGAVGTMISFFTISTAAI 135	Db 75 SSHLFVSEDLFFFLPYLPLPIIFNAGPQVKKQFFRNFMITLGAVGTMISFFTISTAAI 134	Db 75 SSHLFVSEDLFFFLPYLPLPIIFNAGPQVKKQFFRNFMITLGAVGTMISFFTISTAAI 134
Qy	136 SRMNIGITLDVGDFGLAIGAIFSATDSVCTLOVLYNQDETFPLFLYSLVGEVVNDATSVLN 195	Qy 133 AIFSMNIGITLDVGDFGLAIGAIFSATDSVCTLOVLYNQDETFPLFLYSLVGEVVNDATSV 192	Qy 133 AIFSMNIGITLDVGDFGLAIGAIFSATDSVCTLOVLYNQDETFPLFLYSLVGEVVNDATSV 192
Db	136 KHLIDIDPLDFGYLAIGAIFSATDSVCTLOVLYNQDETFPLFLYSLVGEVVNDATSVLN 195	Db 135 ATFORMDISLELDGDLLAIGAIFATDSVCTLOVLYNQDETFPLFLYSLVGEVVNDATSVV 194	Db 135 ATFORMDISLELDGDLLAIGAIFATDSVCTLOVLYNQDETFPLFLYSLVGEVVNDATSVV 194
Qy	196 ALONFDLVHDAAVVULKFLGNFFYLFLSSTPLFLYSLVGEVVNDATSVLN 255	Qy 193 LFNALQNFOLVHDAAVVULKFLGNFFYLFLSSTPLFLYSLVGEVVNDATSV 252	Qy 193 LFNALQNFOLVHDAAVVULKFLGNFFYLFLSSTPLFLYSLVGEVVNDATSV 252
Db	196 AIQSFDMTSDFPKIGLFLYFLSIGNFLYLPSTSPLFLYSLVGEVVNDATSVLN 255	Db 195 LFNAQNFDLTHTRIAPOFGGNFLYLPFASTPLGATVLLGSLAYVIRKLKYFERHSTRE 254	Db 195 LFNAQNFDLTHTRIAPOFGGNFLYLPFASTPLGATVLLGSLAYVIRKLKYFERHSTRE 254
Qy	256 NMMLMAYLSYMIAELLDISGLTIVFEGVIMSYHTHNVNTESSRVTKHAPATLSPIAETF 315	Qy 253 VALMMJMAVLSYMIAELLDISGLTIVFEGVIMSYHTHNVNTESSRVTKHAPATLSPIA 312	Qy 253 VALMMJMAVLSYMIAELLDISGLTIVFEGVIMSYHTHNVNTESSRVTKHAPATLSPIA 312
Db	256 NMMLMAYLSYMIAELFLYLSLPLKIGLFLYFLSIGNFLYLPSTSPLFLYSLVGEVVNDATSVLN 255	Db 255 VALMMJMAVLSYMIAELFLYLSLPLKIGLFLYFLSIGNFLYLPSTSPLFLYSLVGEVVNDATSV 314	Db 255 VALMMJMAVLSYMIAELFLYLSLPLKIGLFLYFLSIGNFLYLPSTSPLFLYSLVGEVVNDATSV 314
Qy	316 LFLEVGMADLTKEWPAFSDRGKSIGISSTILLGLVLGRAFVEPLFSLSNLNTKAPNE 375	Qy 313 ETFLFLYGMADLTKEWPAFSDRGKSIGISSTILLGLVLGRAFVEPLFSLSNLNTKKA 372	Qy 313 ETFLFLYGMADLTKEWPAFSDRGKSIGISSTILLGLVLGRAFVEPLFSLSNLNTKKA 372
Db	316 LFLEVGMADLTKEWPAFSDRGKSIGISSTILLGLVLGRAFVEPLFSLSNLNTKAPNE 375	Db 315 ETFLFLYGMADLTKEWPAFSDRGKSIGISSTILLGLVLGRAFVEPLFSLSNLNTKKA 374	Db 315 ETFLFLYGMADLTKEWPAFSDRGKSIGISSTILLGLVLGRAFVEPLFSLSNLNTKKA 374
Qy	376 KITWRQOQVVIWAGLMRGAVALAYNKFTRSQHTOLQHGNAIMITSTTVVLFSTMVFGM 435	Qy 373 PNEKTFTWROQQVVIWAGLMRGAVALAYNKFTRSQHTOLQHGNAIMITSTTVVLFSTMV 432	Qy 373 PNEKTFTWROQQVVIWAGLMRGAVALAYNKFTRSQHTOLQHGNAIMITSTTVVLFSTMV 432
Db	376 KISFRQQIIWAGLMRGAVALAYNKFTRSQHTOLQHGNAIMITSTTVVLFSTMVFGM 435	Db 375 NSEKTFNQQLIVIWAGLMRGAVALAYNKFTRSQHTOLQHGNAIMITSTTVVLFSTMV 434	Db 375 NSEKTFNQQLIVIWAGLMRGAVALAYNKFTRSQHTOLQHGNAIMITSTTVVLFSTMV 434
Qy	436 MTKPLIRLLP---ASGHP---VTESEPPSSPKSLHSPPLTSMOGSDLESTT-NIVRPPS 486	Qy 433 FGMMTKPLIRLLPASGH---PVTESEPPSSPKSLHSPPLTSMOGSDLESTTN----- 480	Qy 433 FGMMTKPLIRLLPASGH---PVTESEPPSSPKSLHSPPLTSMOGSDLESTTN----- 480
Db	436 MTKPLINLLPQHKQMSHSSMTSSPSSPHFTPLQDSDM1TGPPEVARTA 495	Db 435 FGLLTKPLIRLLPQPKHFTSASTVSDLGSPKSFSLPLLEDRODSEADLGNDDEBAYPRG 494	Db 435 FGLLTKPLIRLLPQPKHFTSASTVSDLGSPKSFSLPLLEDRODSEADLGNDDEBAYPRG 494
Qy	487 LRMMLTKTHTHVYWKFKDADMMPMFGRGFVPPSPGSPEQS 531	Qy 481 -TVRSSSLRMLTKTHTVHYWRFEDDALMRPMGGRGFVPPSPGSPEQS 531	Qy 481 -TVRSSSLRMLTKTHTVHYWRFEDDALMRPMGGRGFVPPSPGSPEQS 531
Db	496 LRMMLRTTHTVHYWKFKDADMMPMFGRGFVPPSPGSPEQS 540	Db 495 TIARPSTSLRMLNAAHTHTVHYWRFDDYFMRPVFGGRGFVPPSPGSPEQS 546	Db 495 TIARPSTSLRMLNAAHTHTVHYWRFDDYFMRPVFGGRGFVPPSPGSPEQS 546
		RESULT 9 Q9ARH6 PRELIMINARY; PRT; 542 AA.	RESULT 9 Q9ARH6 PRELIMINARY; PRT; 542 AA.
RESULT 8		AC Q9ARH6; PRELIMINARY;	AC Q9ARH6; PRELIMINARY;
ID Q94K25		DT 01-JUN-2001 (TREMBLrel. 17, Created)	DT 01-JUN-2001 (TREMBLrel. 17, Created)
AC Q94K25		DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)		DE Sodium/proton exchanger.	DE Sodium/proton exchanger.
DE Sodium/proton exchanger.		OS Citrus paradisi (Grapefruit).	OS Citrus paradisi (Grapefruit).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Magnoliophyta; eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.		OC Magnoliophyta; eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.	OC Magnoliophyta; eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=37656;		{1}	{1}
RN SEQUENCE FROM N.A.		SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RP		PRELIMINARY;	PRELIMINARY;
RC		PRT;	PRT;
TISSUE#PEEL:			
RC			
RA			
RT			
"A heat treatment induced the transcription of a sodium proton			

RT	function in cation detoxification in yeast.;"
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDJB databases
DR	EMBL; AY028416; AAK27314.2; -;
DR	InterPro; IPR001179; FKBP_PPIase.
DR	InterPro; IPR004709; Nah_Exchangers.
DR	InterPro; IPR00676; Nah_Exchanger.
DR	PFam; PF00599; Na <sup>+</sup> _Exchanger_1.
DR	PRINTS; PRO1084; NAHXCHNRR.
DR	TIGRFAMS; TIGR00840; b_cpx1_1;
DR	PROSITE; PS00452; FKBP_PPIASE_1;
SEQ	SEQUENCE 542 AA; 59836 MW; 1A8525F2C5FAEEEC CRC64;
Query Match	75.1%; Score 2043; DB 10; Length 542;
Best Local Similarity	74.3%; Pred. No. 9.3e-143;
Matches	394; Conservative 57; Mismatches 71; Indels 8; Gaps 4;
Qy	13 SHLFWFSEDLFFTYLLPPLIFENAGFQVKKKQFFRNEMTITLGAVGTMISFFTISIAAI 132
Db	74 SHLFWFSEDLFFTYLLPPLIFENAGFQVKKKQFFRNEMTITLGAVGTMISFFTISIAAI 133
Qy	133 AIFSRMNIGIPLDVGFELAIALIFATSDVCTQLQVNQDETFPLFLSVLVEGRGVNDATSV 192
Db	134 QFFKLDIGTDIDGYLAIGAIFAATDSVCTQLQVNQDDTFLYSVLFVGIVLGVNNDATSV 193
Qy	193 LFNALQNFDLVHDAAVLVLKFLGNNFLYLFSLTLGVFAGLSAYTIKKYIGRHSTDRE 252
Db	194 LENA.LQSFDTLTHINRSAFOLIGNFLYLPFLSTLGVIGLGSAVVIKKYIGRHSTDRE 253
Qy	253 VALMMILMAYLISYMLAELDLSGILTVEFGCIVVMSHYTWNVTESSRVTTKHAFTLSETA 312
Db	254 VAIVMLMAYLISYMLAELFLYLSGILTVEFGCIVVMSHYTWNVTESSRVTTKHAFTLSETA 313
Qy	313 ETFLFLYGVGMDALDEKWEFASDRPGKSIGISSLLGVLIGRAAFVPLFLSFLSNLTKA 372
Db	314 EIFTFLYGVGMDALDEKWEFASDRPGKSIGISSLLGVLIGRAAFVPLFLSFLTNLAKKS 373
Qy	373 PNEKITWQOVIVIWAGLARGAVSTALANKFTTSQHTQLHGNAIMITSTITVVLFSIMV 432
Db	374 PTEKISIKQOQVIVIWAGLNRGAWSMALAYNQTFRGTHQLRENAIMITSTITVVLFSIVV 433
Qy	433 FGMMTKPLTRLLPASGHP --VTPSPSKPLHSPLTSQMG --SDLESITNIVRPS 486
Db	434 FGLTEPLRLLHPKPKHTNHLISDPSTPKSLSQLLEGGQDSYADLVGPT -VPRPGS 492
Qy	487 LRMLLTKPTHTVHYWRKFDDALMRPMFGRGFYFSPGSPTEQS -HGGR 535
Db	493 LRALLTPPTHTVHYWRKFDDALMRPMFGRGFYFSPGSPTEQSVRGGQ 542
RESULT 10	RESULT 11
O9ZPK3	SEQUENCE FROM N.A.
ID	PRELIMINARY; PRT; 538 AA.
AC	Q94LX3 PRELIMINARY; PRT; 555 AA.
DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE	Sodium proton exchanger NHX1 (Fragment).
GN	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=CV_COLUMBIA;
RC	MEDLINE=9145575; Pubmed=9990049;
RX	Gaxiola R.A., Rao R., Sherman A., Grisafi P., Alper S.L., Fink G.R.;
RA	"The Arabidopsis thaliana proton transporters, AtNHX1 and Avp1, can
RT	Torenia hybrida.
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC	Asteridae; euasterids I; Lamiales; Lamiales incertae sedis; Toreniae;





(2) SEQUENCE FROM N.A.  
 RP SPAIN-EV. COLUMBIA;  
 RC Wash-U;  
 RA "The A. thaliana Genome Sequencing Project.";  
 RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RL [3] SEQUENCE FROM N.A.  
 RN RP SPAIN-EV . COLUMBIA;  
 RA Waterston R.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF007271; AAB61069\_1;  
 DR InterPro: IPR001179; FKBP\_PPIase.  
 DR InterPro: IPR000676; NAD\_Exchanger.  
 DR Pfam: PF00999; Na\_H\_Exchanger\_1.  
 DR PROSITE: PS00453; FKBP\_PPINSE\_1; UNKNOWN\_1.  
 DR PROSITE: PS00453; FKBP\_PPINSE\_1; UNKNOWN\_1.  
 SQ SEQUENCE 457 AA: 50611 MW: 0AF2P235F1A258EE CRC64:

Query	Match	Score	Length
	62.4%	1698.5	457;
Matches	333; Conservative	74.0%; Pred.	Length 457;
Qy	3 MEVAALARIGALYTTSDYASVVSINLEVALGACTIVLGHILEENRNNNESTALIIGLCIG 62	Mismatches	51; Indels 21; Gaps 3;
Db	2 LDSLVSKPLSL_STDSHSSVALNLVALLGACIVLGHILEENRNNNESTALIIGLCIG 60		
Qy	63 VVILLMTKGKSSHFLYPSEDLFIFYLPPILENAGFOVKKKOFFRNEMITLFGAVGTM 122		
Db	61 VTLILISGKSSHLVPSEDLFIFYLPPILENAGQVKKQQFRNEVTIMLFGAVGT 120		
Qy	123 SFTTISTIAIAFSRMNIGTLDVGDFLAIGAFLSAFDVSCTLQLVNQDETPFLYSLVRE 182		
Db	121 SFTTISLGVTOFFKKLDTGTFDGYLAIGAFAATDSCTLQLVNQDETPFLYSLVGE 180		
Qy	183 GVNDATSVLENALQNDLVHDAAVVLFGLNFYFLSSTFLCV-----F 230		
Db	181 GVNDATSVVNAIQSFDLTHUNHEAAFLGNFLYFLFLSTLGAASVLFLSSLPFL 240		
Qy	231 AGLSAYLIKLYIG-----RHSTDREVALMMLMAYLSYMLAELDLISGILTIVFFCG 282		
Db	241 TGLISAYTIKKLYFGRWHEINGCHRSTDREVALMMLMAYLSYMLAELDLISGILTIVFFCG 300		
Qy	283 IVMSHYTWHNVTESSRVTKHAFATLSFIAETFLFLYGMDALDTEKWEFASDRPGKSIG 342		
Db	301 IVMSHYTWHNVTESSRITKHFATLSFIAETFLFLYGMDALDTEKWSVSDPTPSIA 360		
Qy	343 ISSILGLVLGRAAFYFPLSFLSNLTKAPNEKITWQQVVIWAGLMRCAVSTALAYN 402		
Db	361 VSSLMLGMVGMVGRAAFYFPLSFLSNLAKKNOSEKINFNMQVVIWWSGLMRCAVSMALAYN 420		
Qy	403 KFRSRGHTQLHGNAIMITSTTVCLFSTMV 432		
Db	421 KFRAGHPDVRGNAIMITSTTVCLFSTVV 450		

Search completed: March 26, 2003, 18:53:48  
 Job time : 41 secs

